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(54) **SINGLE CHAIN TRAIL FUSION POLYPEPTIDES AND ENCODING NUCLEIC ACIDS**

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Related U.S. Application Data

(63) Continuation of application No. 13/902,328, filed on May 24, 2013, now Pat. No. 8,921,519, which is a continuation of application No. 13/055,109, filed as application No. PCT/EP2009/059269 on Jul. 18, 2009, now Pat. No. 8,450,460.

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C07K 16/00 (2006.01)
C12N 15/62 (2006.01)
C12N 15/79 (2006.01)

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CPC **C07K 14/525** (2013.01); **C07K 16/00** (2013.01); **C12N 15/62** (2013.01); **C12N 15/79**

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C07K 2319/00 (2013.01); **C07K 2319/30** (2013.01)

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C07K 2317/52; **C07K 2317/55**; **C07K 2319/00**; **C07K 2319/30**; **C12N 15/62**; **C12N 15/79**

See application file for complete search history.

(56) **References Cited**

U.S. PATENT DOCUMENTS

8,147,843 B2	4/2012	Hill et al.
8,450,460 B2	5/2013	Hill et al.
2004/0014948 A1	1/2004	Halkier et al.
2007/0286843 A1	12/2007	Pfizenmaier et al.
2010/0199364 A1	8/2010	Hill et al.
2015/0126710 A1	5/2015	Hill et al.

FOREIGN PATENT DOCUMENTS

WO WO 2005/103077 11/2005

OTHER PUBLICATIONS

International Search Report for International Application No. PCT/EP2009/059269 with a mailing date of Oct. 29, 2009.
Wajant, et al.; "Tumor Therapeutics by Design: Targeting and Activation of Death Receptors"; Cytokine and Growth Factor Reviews; vol. 16, No. 1, pp. 55-76 (Feb. 1, 2005).

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(57) **ABSTRACT**

The present invention refers to single-chain fusion proteins comprising three soluble TNF superfamily (TNFSF) cytokine domains and nucleic acid molecules encoding these fusion proteins. The fusion proteins are substantially non-aggregating and suitable for therapeutic, diagnostic and/or research applications.

18 Claims, 15 Drawing Sheets

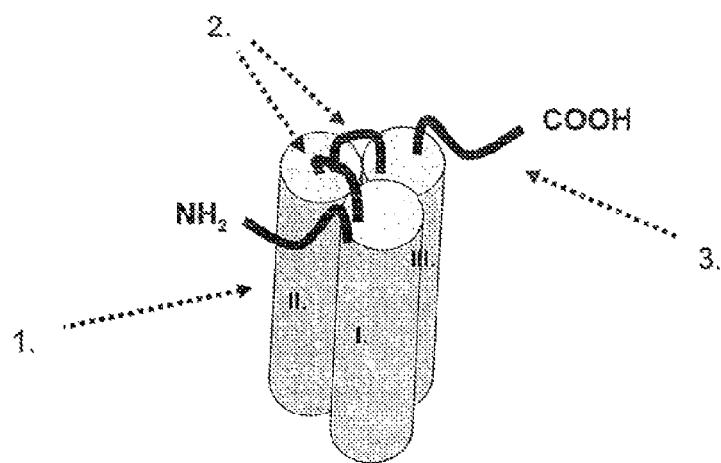
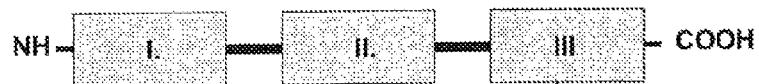
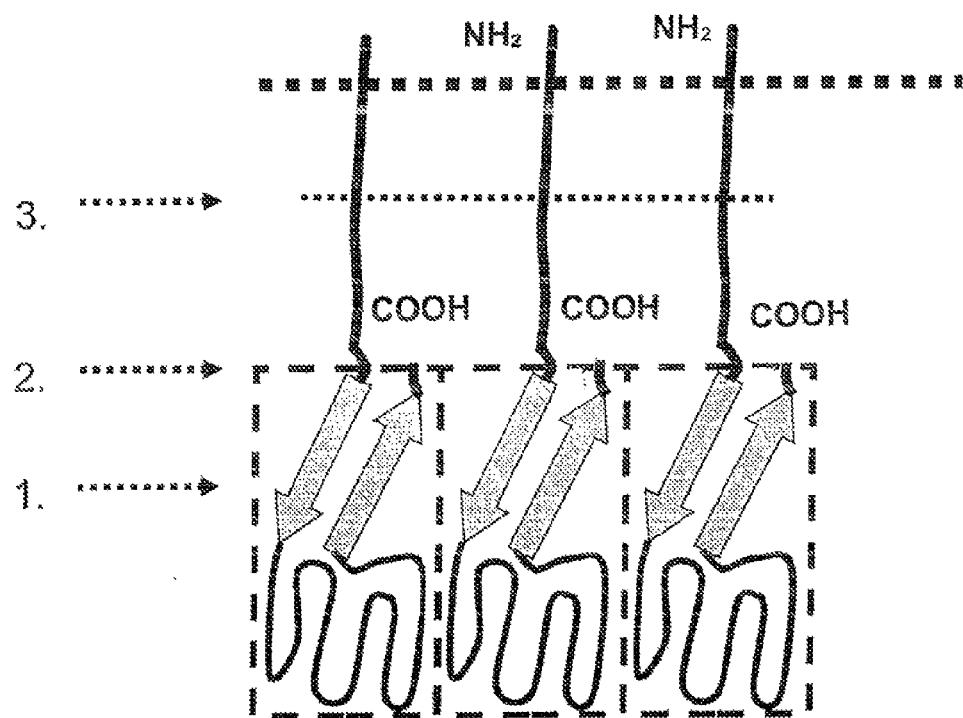
Figure 1**Figure 2**

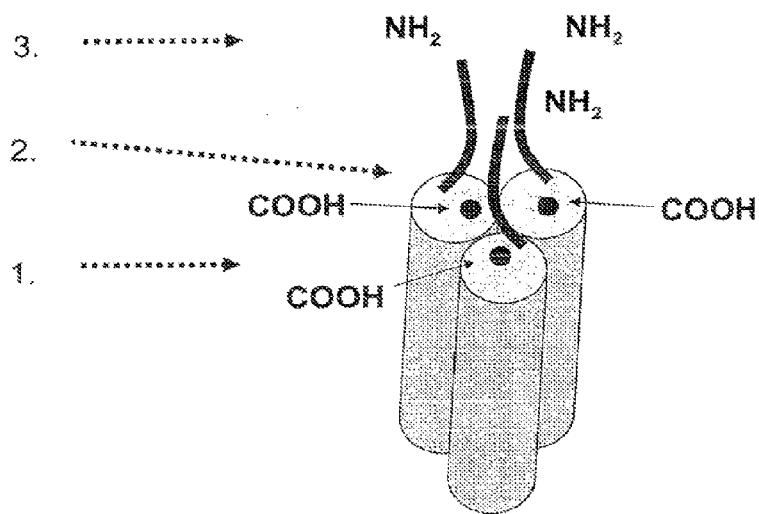
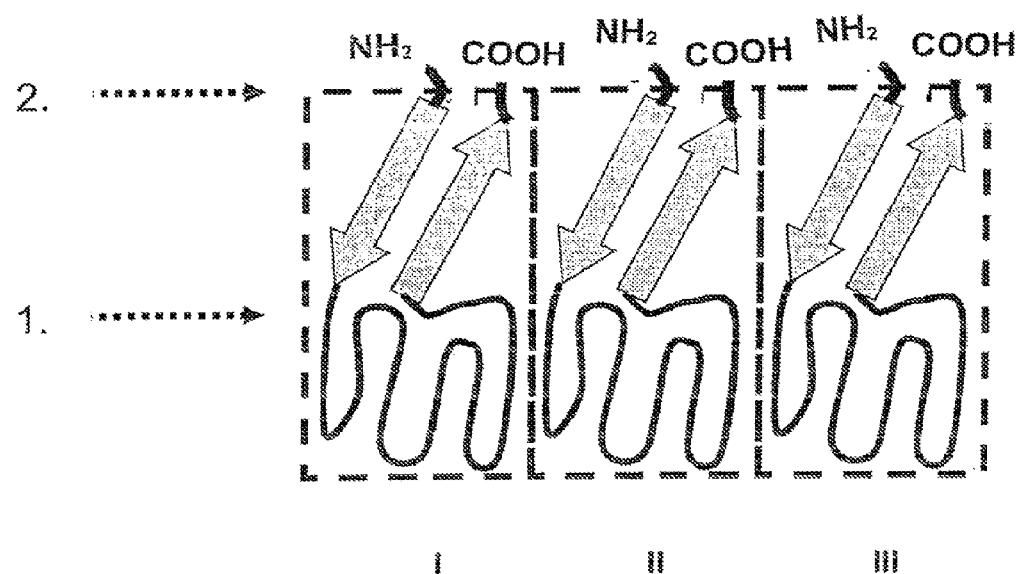
Figure 3**Figure 4**

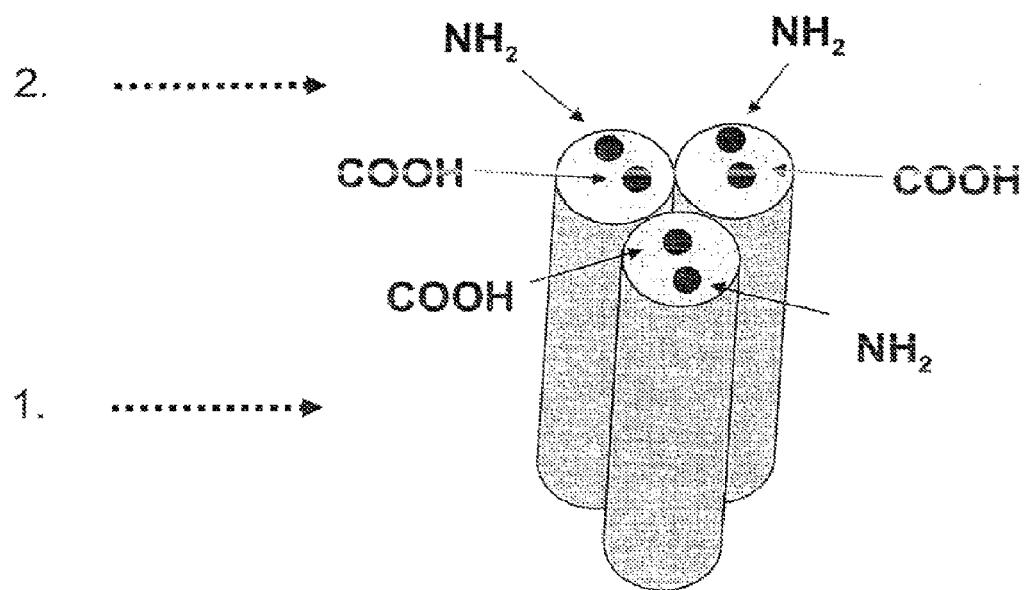
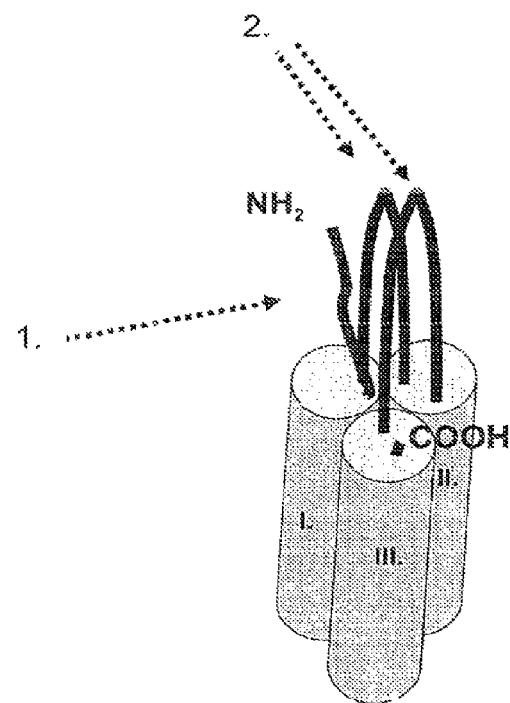
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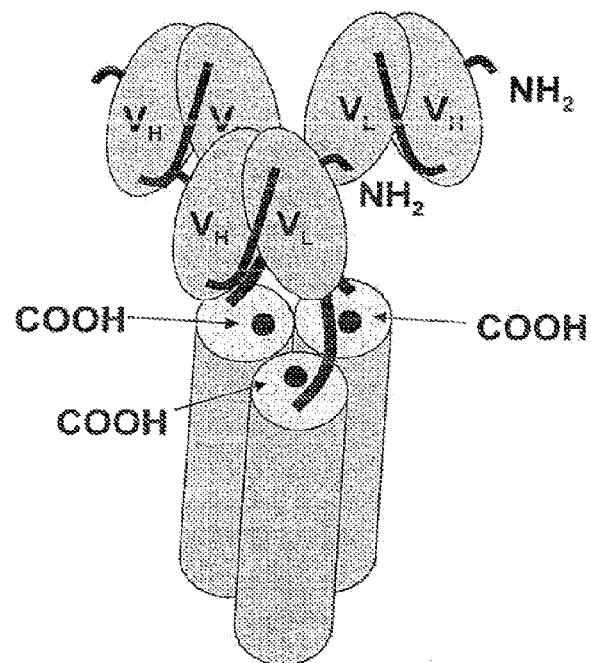
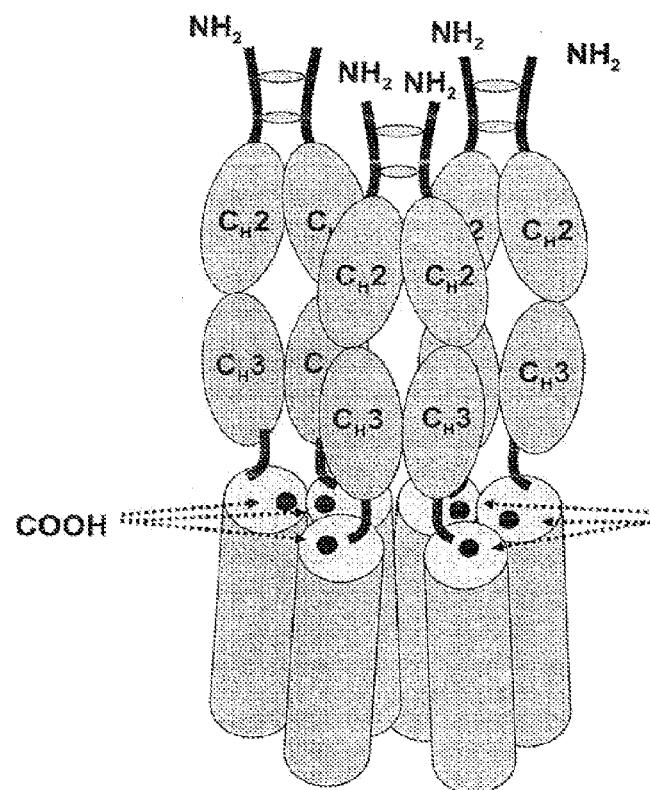
Figure 7**Figure 8**

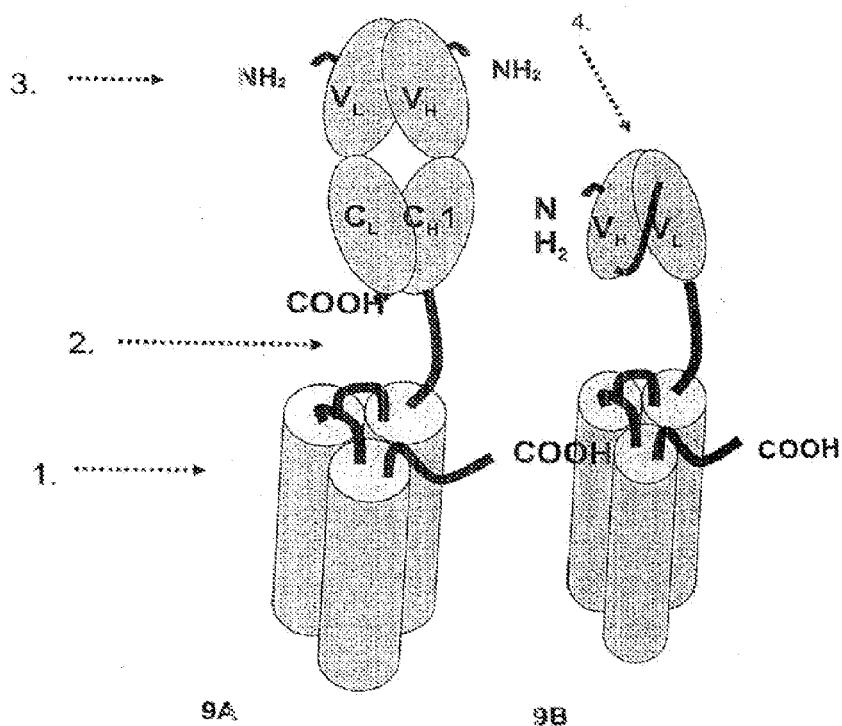
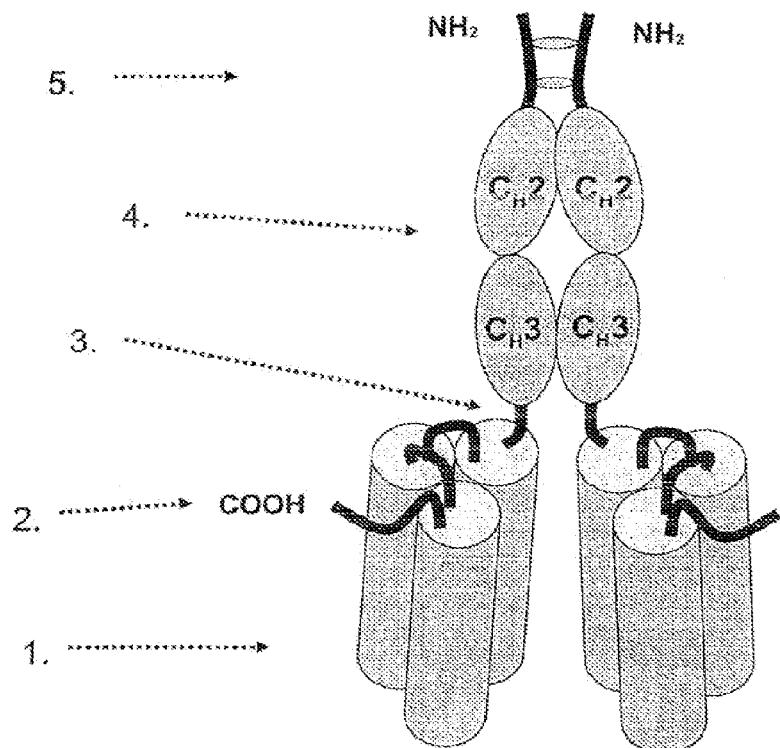
Figure 9**Figure 10**

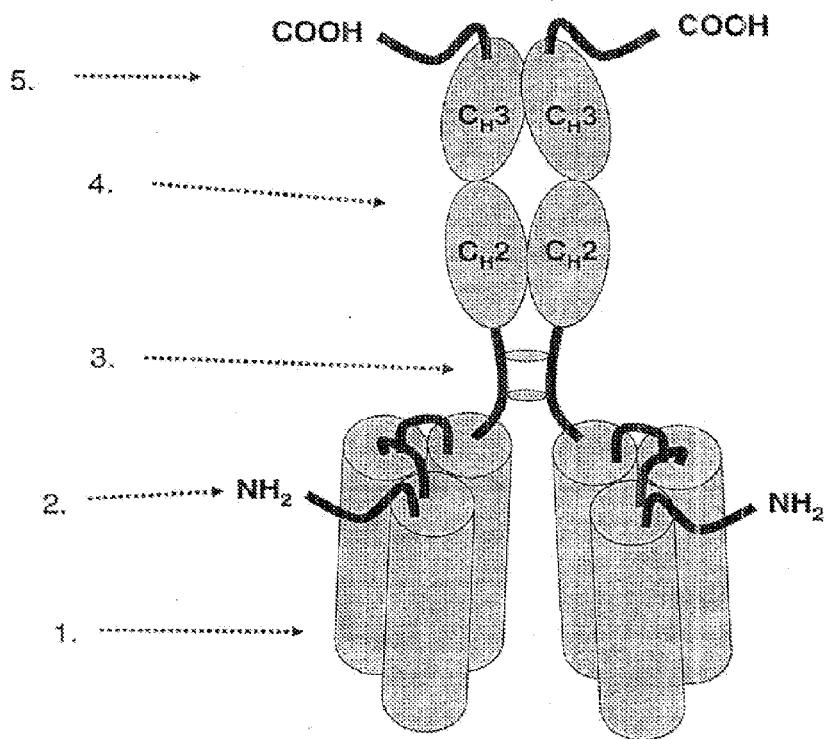
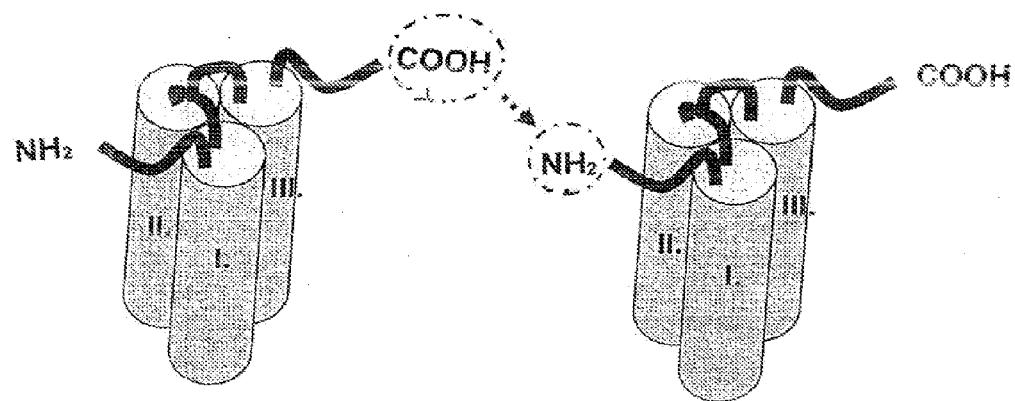
Figure 11**Figure 12**

Figure 13

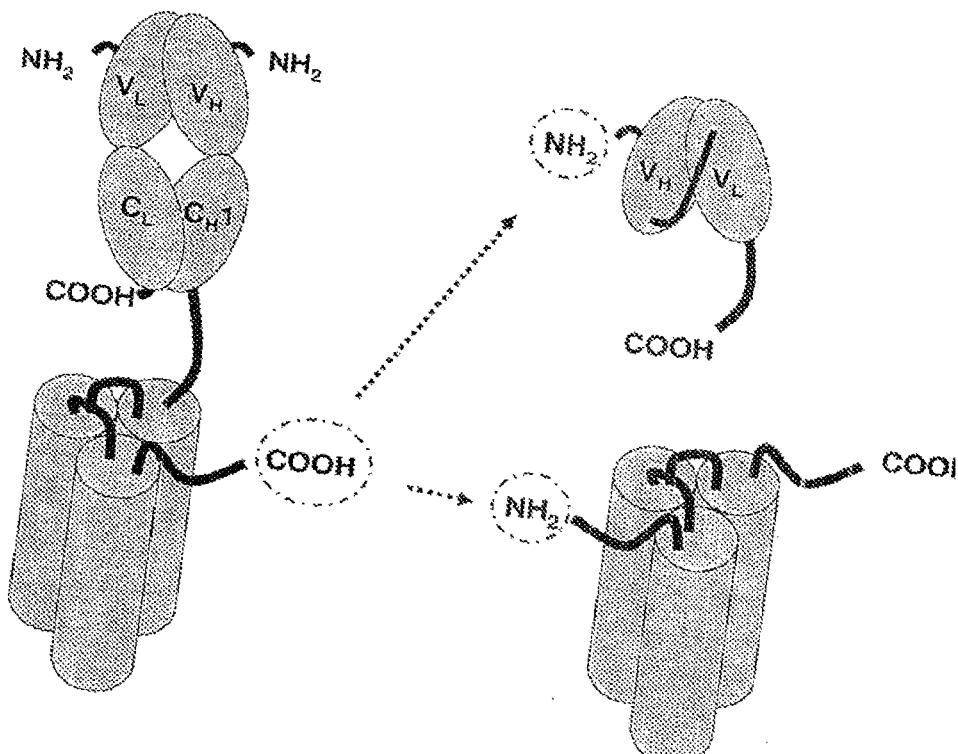


Figure 14

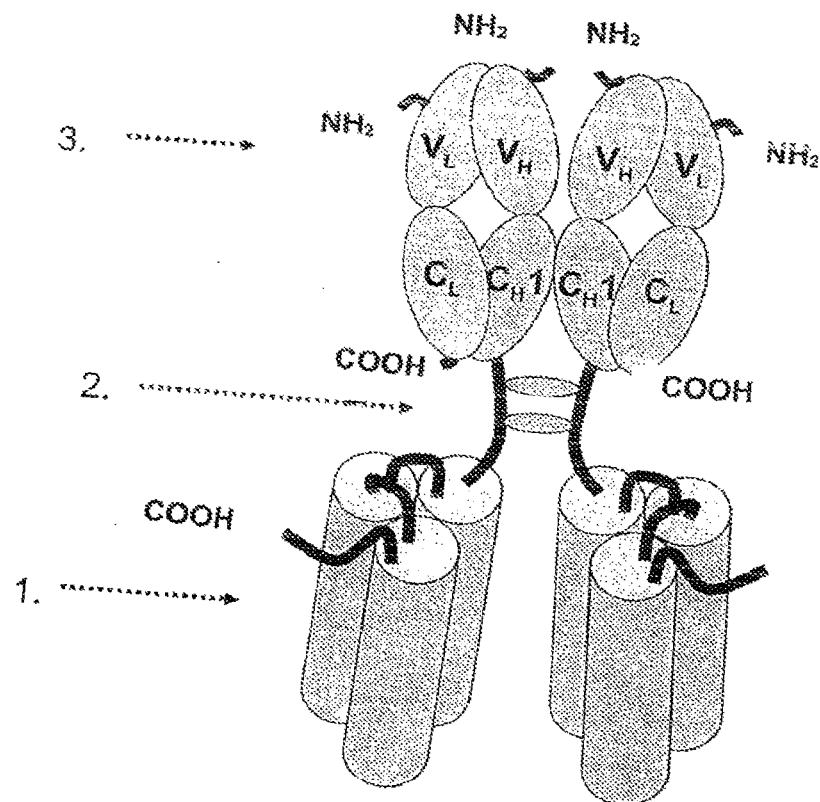


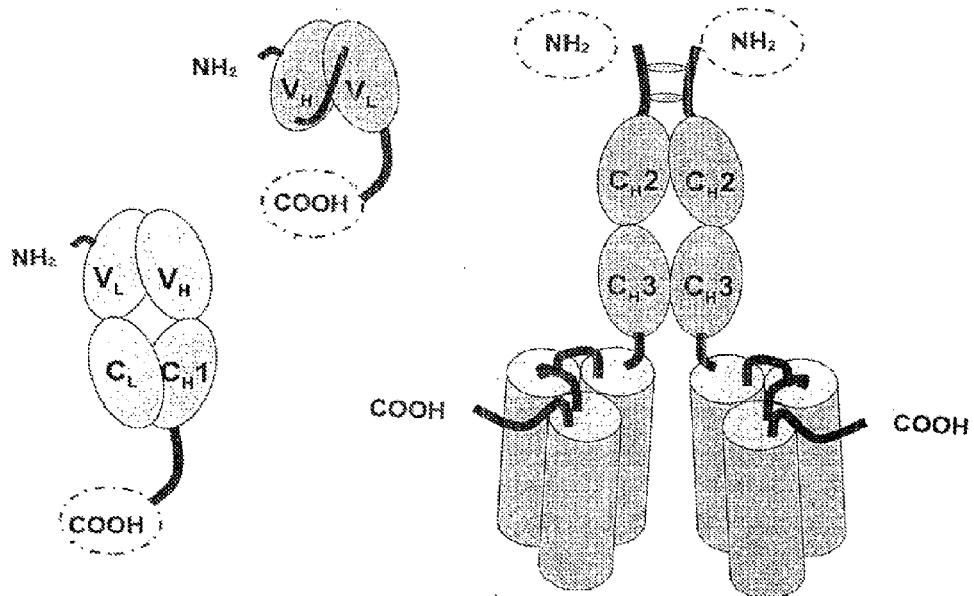
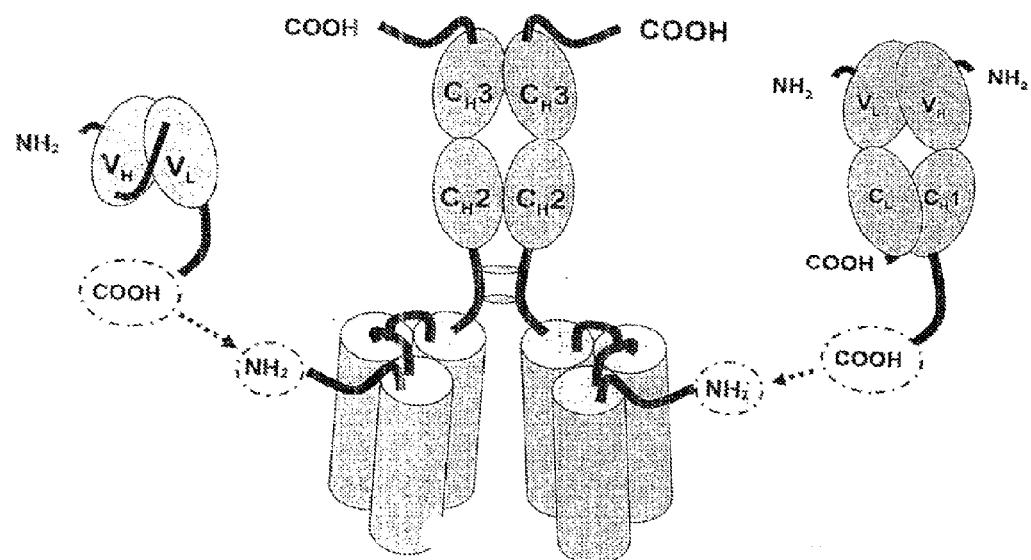
Figure 15**Figure 16**

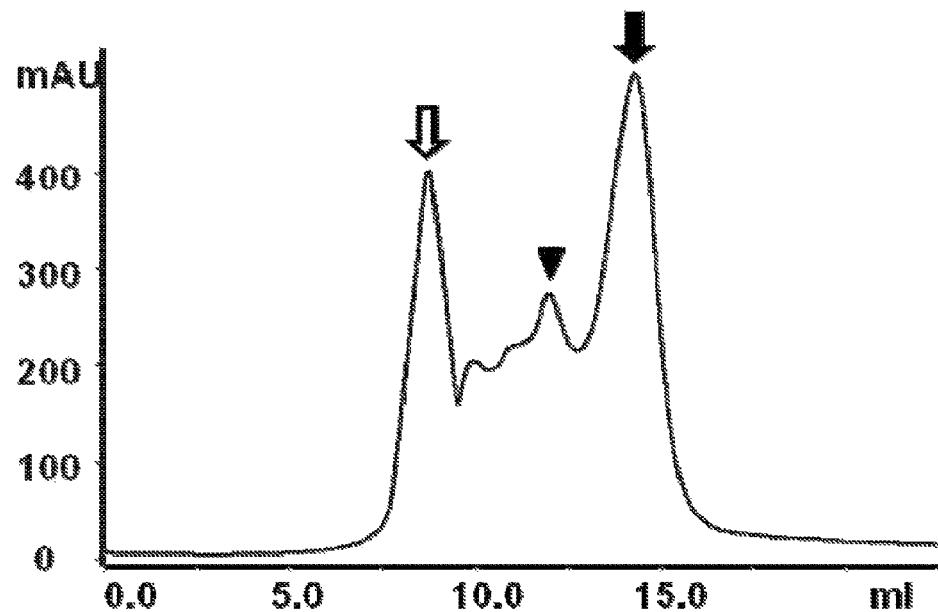
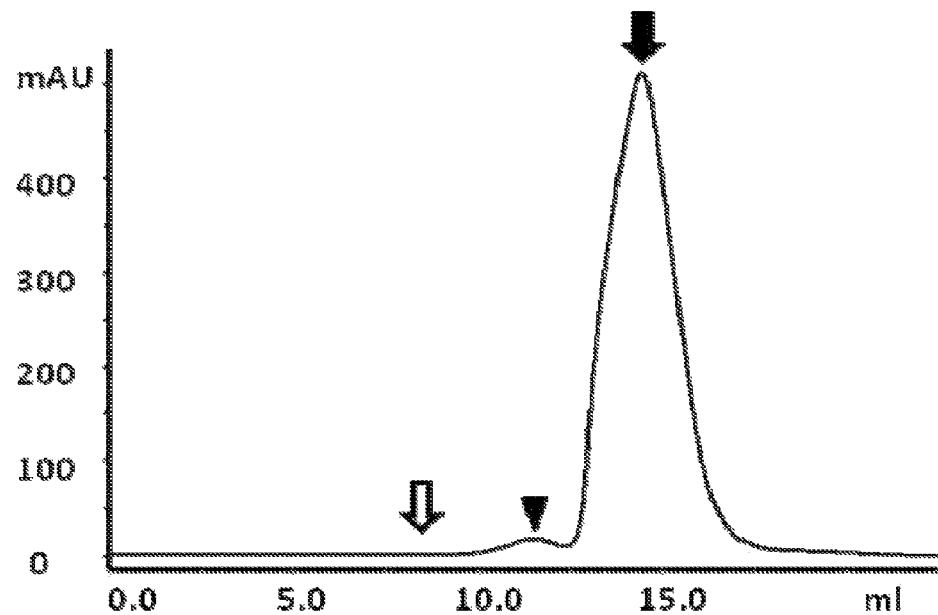
Figure 17**A TNF-SF protein Aggregation****B TNF-SF protein defined soluble protein**

Figure 18

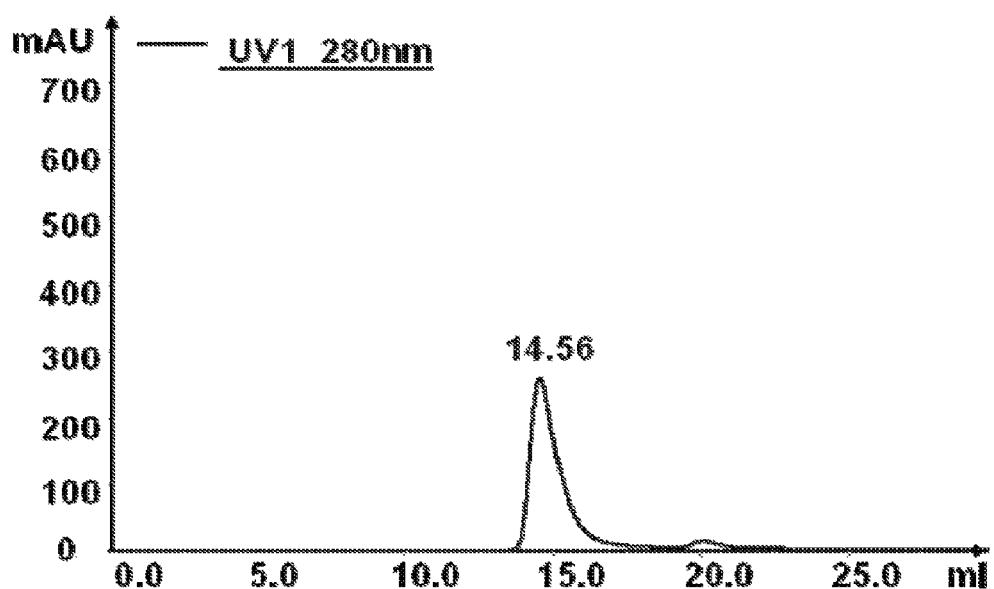


Figure 19

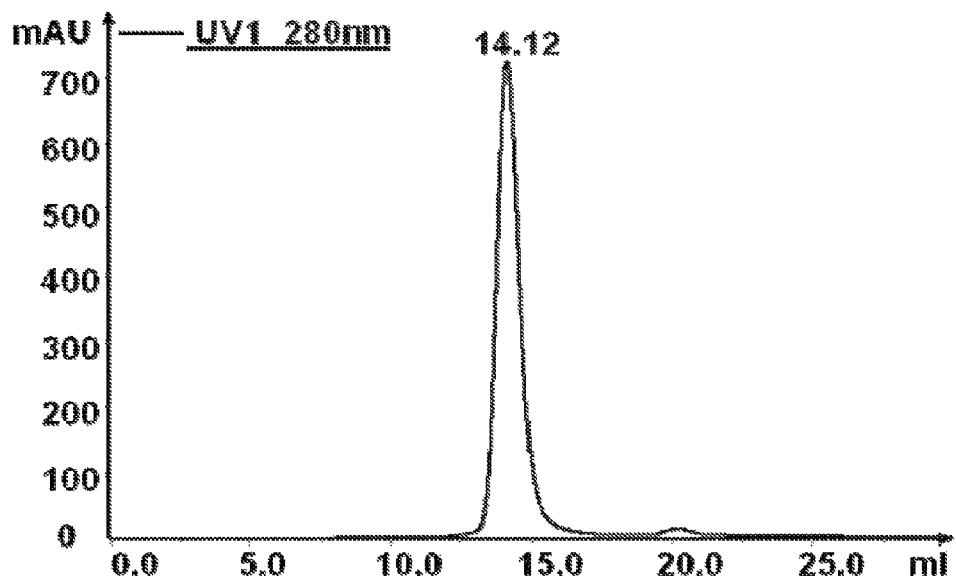
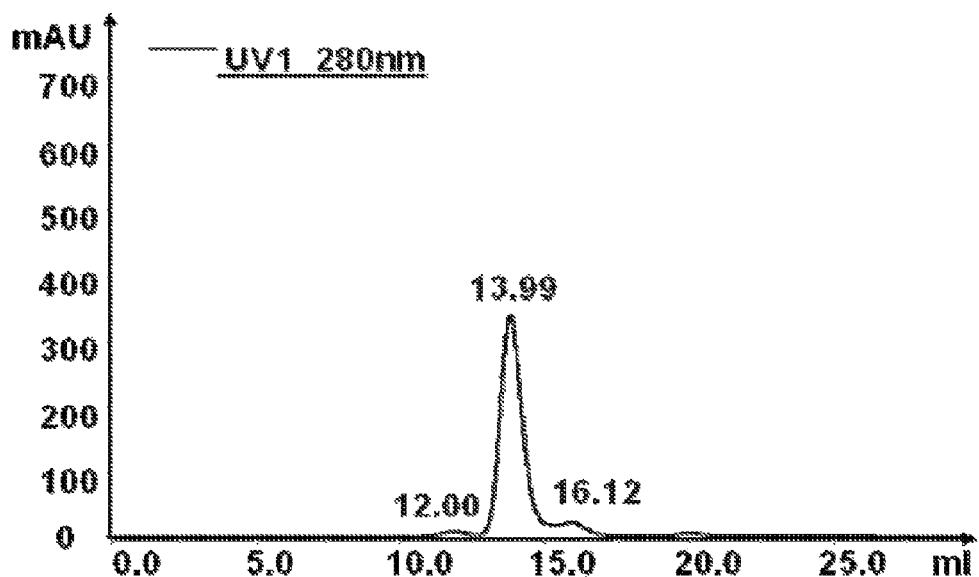
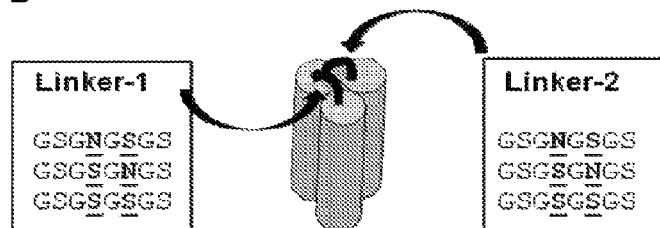
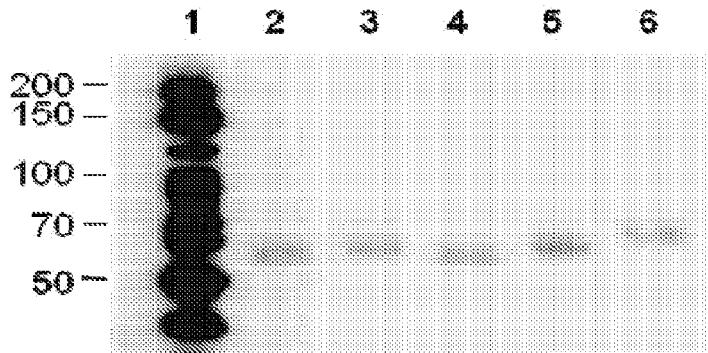


Figure 20**Figure 21****A**

Gly281	1.	2.	Arg121
I.	<u>A</u> G S G N G S G S R		
II.	A G S G <u>S</u> G <u>N</u> G S R		
III.	A G S G S G S G S R		

B**C**

Protein	Linker-layout
scTRAILwt- <u>NNNN</u>	both linkers with Asn in pos-1
scTRAILwt- <u>NNNN</u>	Linker-1 with Asn in pos-1, linker-2 with Asn in pos-2
scTRAILwt- <u>NNSS</u>	Linker-1 with Asn in pos-1, linker-2 with Ser in pos-2
scTRAILwt- <u>NNNS</u>	Linker-1 with Ser in pos-1, linker-2 with Asn in pos-2
scTRAILwt- <u>NNNN</u>	both linkers with Asn in position-2

Figure 22

Lane	Sample	Observed Linker Glycosylation
1	PageRuler, Fermentas	
2	scTRAILwt-NSNS	no linker glycosylation
3	scTRAILwt-NSSN	<i>Linker-2 position-2 glycosylated</i>
4	scTRAILwt-NSSS	no linker glycosylation
5	scTRAILwt-SNNS	<i>Linker-1 position-2 glycosylated</i>
6	scTRAILwt-SNSN	<i>Linker-1 and Linker-2 position-2 glycosylated</i>

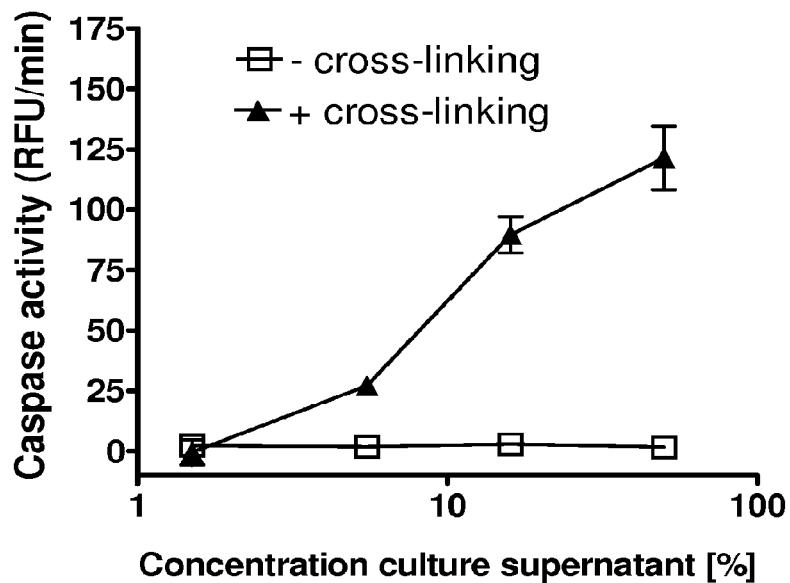
Figure 23

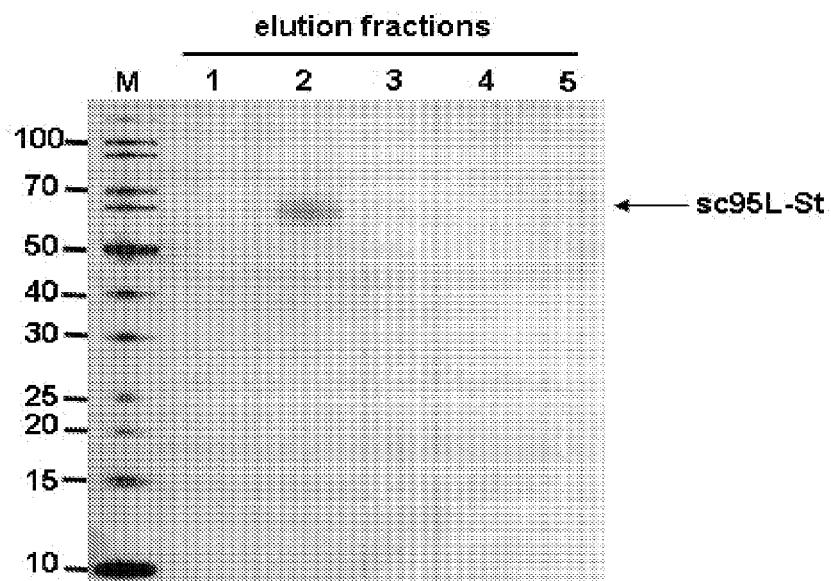
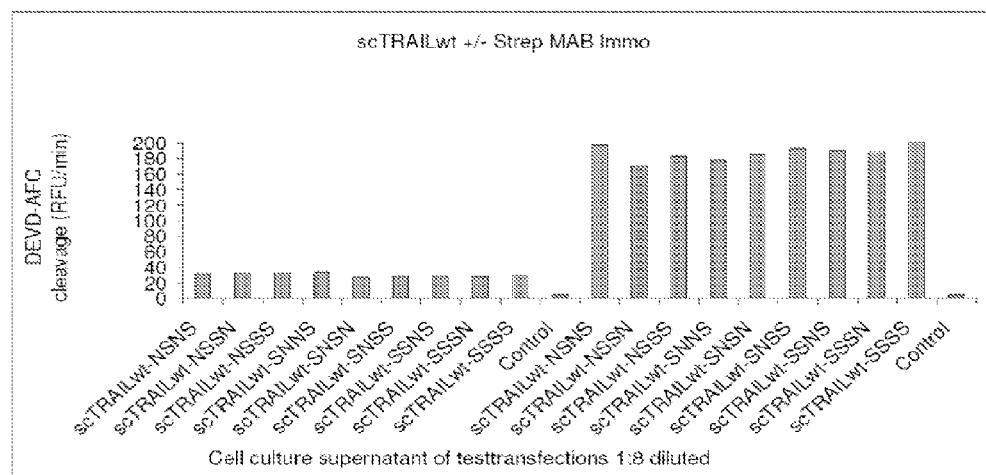
Figure 24**Figure 25**

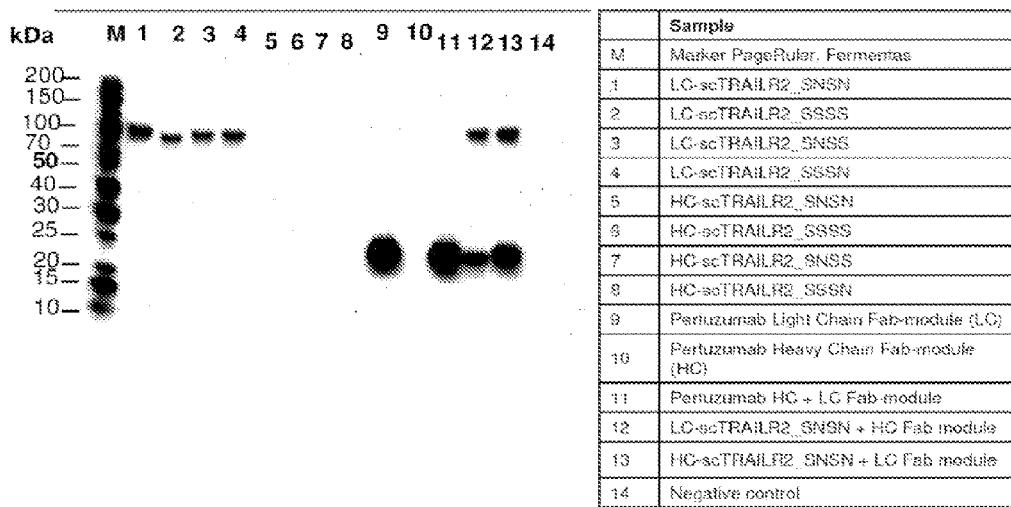
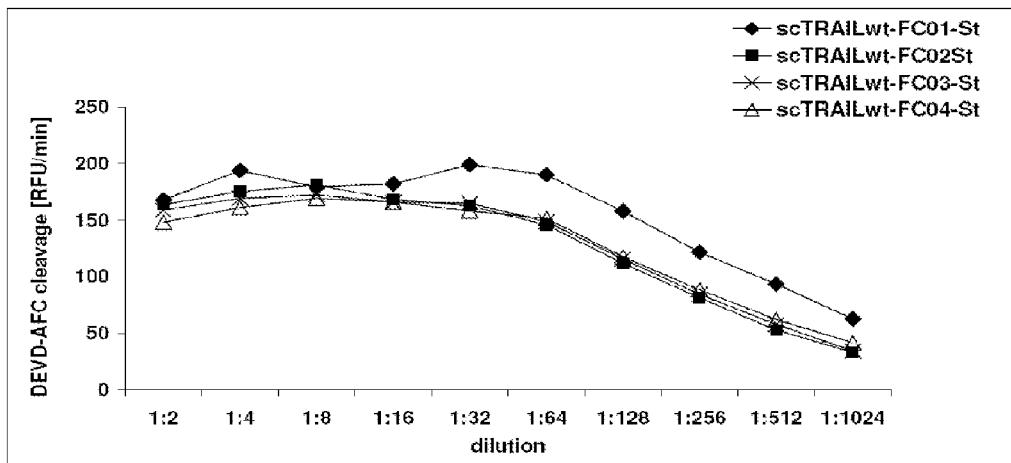
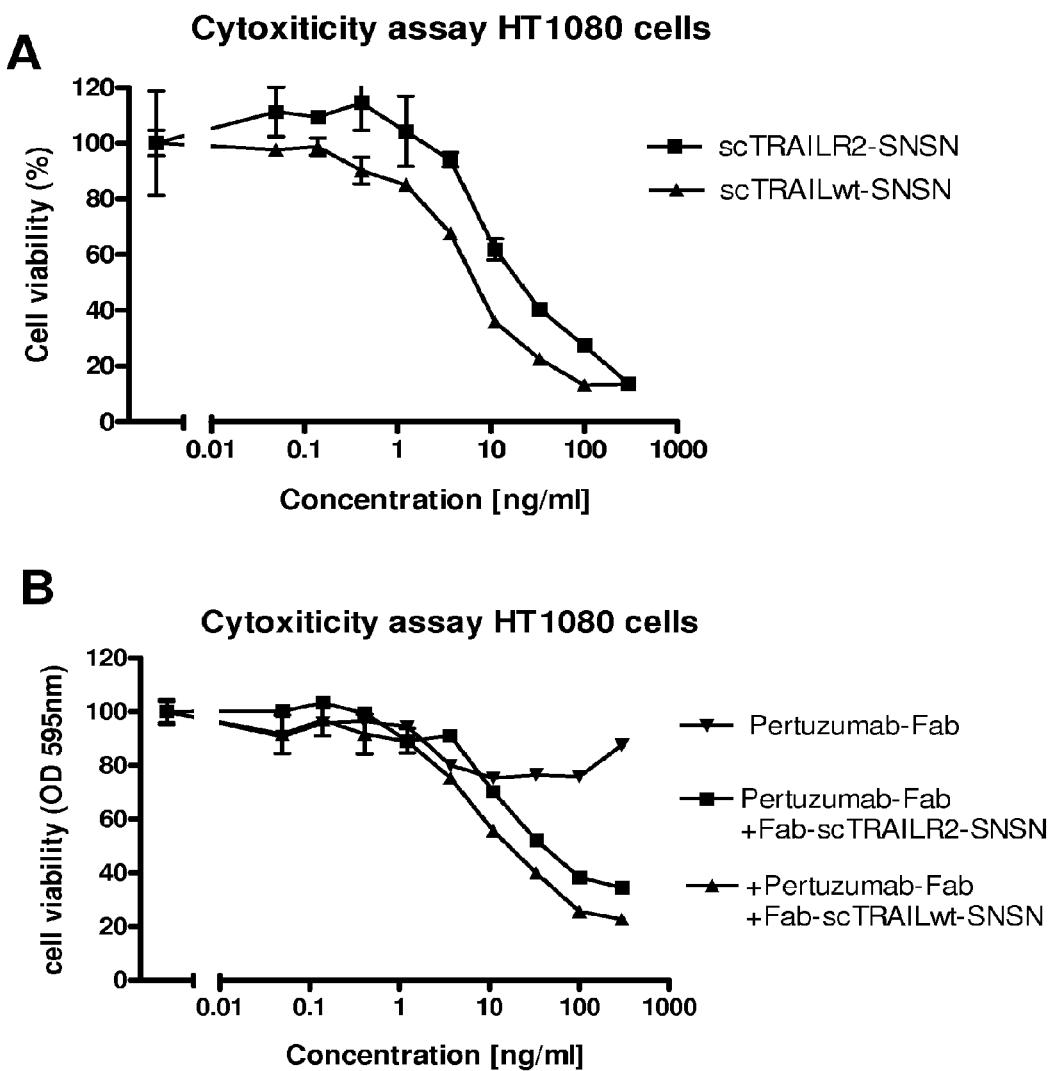
Figure 26**Figure 27**

Figure 28



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**SINGLE CHAIN TRAIL FUSION
POLYPEPTIDES AND ENCODING NUCLEIC
ACIDS**

This application is a continuation of U.S. application Ser. No. 13/902,328, filed May 24, 2013, now U.S. Pat. No. 8,921,519; which is a continuation of U.S. application Ser. No. 13/055,109, filed Mar. 10, 2011, now U.S. Pat. No. 8,450,460; which is a National Stage of International Application PCT/EP2009/059269, filed Jul. 18, 2009, published Jan. 28, 2010, under PCT Article 21(2) in English; which claims the priority of EP 08013112.1, filed Jul. 21, 2008. The contents of the above applications are incorporated herein by reference in their entirety.

**REFERENCE TO SEQUENCE LISTING, TABLE
OR COMPUTER PROGRAM**

The Sequence Listing is concurrently submitted herewith with the specification as an ASCII formatted text file via EFS-Web with a file name of Sequence_Listing.txt with a creation date of Jun. 30, 2014, and a size of 154 kilobytes. The Sequence Listing filed via EFS-Web is part of the specification and is hereby incorporated in its entirety by reference herein.

DESCRIPTION

The present invention refers to single-chain fusion proteins comprising three soluble TNF superfamily (TNFSF) cytokine domains and nucleic acid molecules encoding the fusion proteins. The fusion proteins are substantially non-aggregating and suitable for therapeutic, diagnostic and/or research applications.

STATE OF THE ART

It is known that trimerisation of TNFSF cytokines, e.g., the CD95 ligand (CD95L), is required for efficient receptor binding and activation. Trimeric complexes of TNF superfamily cytokines, however, are difficult to prepare from recombinant monomeric units.

WO 01/49866 and WO 02/09055 disclose recombinant fusion proteins comprising a TNF cytokine and a multimerisation component, particularly a protein from the C1q protein family or a collectin. A disadvantage of these fusion proteins is, however, that the trimerisation domain usually has a large molecular weight and/or that the trimerisation is rather inefficient. Schneider et al. (J Exp Med 187 (1989), 1205-1213) describe that trimers of TNF cytokines are stabilised by N-terminally positioned stabilisation motifs. In CD95L, the stabilisation of the receptor binding domain trimer is presumably caused by N-terminal amino acid domains which are located near the cytoplasmic membrane.

Shiraishi et al. (Biochem Biophys Res Commun 322 (2004), 197-202) describe that the receptor binding domain of CD95L may be stabilised by N-terminally positioned artificial α -helical coiled-coil (leucine zipper) motifs. It was found, however, that the orientation of the polypeptide chains to each other, e.g. parallel or antiparallel orientation, can hardly be predicted. Further, the optimal number of heptad-repeats in the coiled-coil zipper motif are difficult to determine. In addition, coiled-coil structures have the tendency to form macromolecular aggregates after alteration of pH and/or ionic strength.

WO 01/25277 relates to single-chain oligomeric polypeptides which bind to an extracellular ligand binding domain of

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a cellular receptor, wherein the polypeptide comprises at least three receptor binding sites of which at least one is capable of binding to a ligand binding domain of the cellular receptor and at least one is incapable of effectively binding to a ligand binding domain of the cellular receptor, whereby the single-chain oligomeric polypeptides are capable of binding to the receptor, but incapable of activating the receptor. For example, the monomers are derived from cytokine ligands of the TNF family, particularly from TNF- α .

WO 2005/103077 discloses single-chain fusion polypeptides comprising at least three monomers of a TNF family ligand member and at least two peptide linkers that link the monomers of the TNF ligand family members to one another. Recent experiments, however, have shown that these single-chain fusion polypeptides show undesired aggregation.

It was an object of the present invention to provide single-chain fusion proteins comprising at least three TNF cytokine domains which allow efficient recombinant manufacturing combined with good stability concerning aggregation.

SUMMARY OF THE INVENTION

The present invention relates to a single-chain fusion polypeptide comprising:

- (i) a first soluble TNF-family cytokine domain,
- (ii) a first peptide linker,
- (iii) a second soluble TNF-family cytokine domain,
- (iv) a second peptide linker, and
- (v) a third soluble TNF-family cytokine domain,

which is substantially non-aggregating.

The invention further relates to a nucleic acid molecule encoding a fusion protein as described herein and to a cell or a non-human organism transformed or transfected with a nucleic acid molecule as described herein.

The invention also relates to a pharmaceutical or diagnostic composition comprising as an active agent a fusion protein, a nucleic acid molecule, or a cell as described herein.

The invention also relates to a fusion protein, a nucleic acid molecule, or a cell as described herein for use in therapy, e.g., the use of a fusion protein, a nucleic acid molecule, or a cell as described herein for the preparation of a pharmaceutical composition in the prophylaxis and/or treatment of disorders caused by, associated with and/or accompanied by dysfunction of TNFSF cytokines, particularly proliferative disorders, such as tumours, e.g. solid or lymphatic tumours; infectious diseases; inflammatory diseases; metabolic diseases; autoimmune disorders, e.g. rheumatoid and/or arthritic diseases; degenerative diseases, e.g. neurodegenerative diseases such as multiple sclerosis; apoptosis-associated diseases or transplant rejections.

DESCRIPTION OF THE FIGURES

FIG. 1 Domain structure of the inventive single-chain fusion polypeptide. I., II., III. soluble TNF-family cytokine domains.

FIG. 2 Schematic picture representing the general structure of TNF-SF proteins. ■■■ cell membrane, N-terminus located within the cell, 1. anti-parallel β -fold of receptor-binding domain (RBD), 2. interface of RBD and cell membrane, 3. protease cleavage site.

FIG. 3 Schematic picture representing the structure of the native TNF-SF trimer. Cylindric structures represent RBDs, N-termini connect RBD with the cell membrane.

FIG. 4 Schematic picture representing the structure of three soluble domains comprising the receptor-binding domain of a TNF cytokine. I., II., III. soluble TNF-family cytokine domains.

FIG. 5 Trimerisation of the soluble domains comprising the RBD of a TNF cytokine, characterised in that the N- and C-termini of the three soluble domains form a surface.

FIG. 6 Schematic picture representing the structure of the single-chain TNF-SF comprising all or a part of the stalk-region illustrating the requirement of longer linkers to compensate for the distance to the N-terminus of the next soluble domain.

FIG. 7 scFv-TNF-SF fusion protein known from the art.

FIG. 8 Fc-TNF-SF fusion protein known from the art.

FIG. 9A Single-chain fusion polypeptide comprising an additional Fab antibody fragment.

FIG. 9B Single-chain fusion polypeptide comprising an additional scFv antibody fragment.

FIG. 10 Dimerization of two N-terminally fused scFc fusion polypeptides via disulfide bridges.

FIG. 11 Dimerization of two C-terminally fused scFc fusion polypeptides via disulfide bridges.

FIG. 12 Dimerization of single-chain fusion polypeptides via a linker.

FIG. 13 Single-chain fusion polypeptide comprising an additional Fab antibody fragment further fused to a second fusion polypeptide or to a scFv fusion polypeptide.

FIG. 14 Dimerization of two scFab fusion polypeptides via disulfide bridges.

FIG. 15 N-terminally fused scFc fusion polypeptides further comprising a Fv and/or Fab antibody fragment.

FIG. 16 C-terminally fused scFc fusion polypeptides further comprising a Fv and/or Fab antibody fragment.

FIG. 17 SEC analysis of recombinantly expressed, purified TNF-SF members under native conditions. Exemplarily shown are two SEC analyses of purified TNF-SF members on a Superdex200 column under native condition (e.g.: PBS, pH 7.4). The diagrams show the absorption at 280 nm (mAU) plotted against the elution volume (ml). The filled arrow indicates the elution peak for the fraction containing defined, soluble trimeric TNF-SF protein. The triangle indicates the elution peak for the oligomerised TNF-SF. The open arrow indicates the void volume of the SEC-column that contains protein-aggregates, which are too big to be separated (>800 kDa).

A: TNF-SF protein Aggregation Diagram A exemplarily shows an analysis of a TNF-SF protein preparation that contains a high amount of oligomerised/aggregated protein (indicated by the high amount of protein eluting in the void volume and the high amount of oligomeric protein).

B: TNF-SF protein defined soluble protein Diagram B exemplarily shows an analysis for a TNF-SF protein preparation that contains almost exclusively defined soluble protein (indicated by the absence of protein eluting in the void volume and by the very limited amount of protein eluting as oligomer).

FIG. 18 SEC analysis of recombinantly expressed, affinity purified Fab-scTRAILR2-SSSS.

SEC analysis of Fab-scTRAILR2-SSSS on a Superdex200 column using PBS, pH 7.4. The diagram shows the absorption at 280 nm (mAU) plotted against the elution volume (ml). The protein elutes as a distinct peak with an elution volume of 14.56 ml, corresponding to an apparent MW of 68 kDa. No additional protein peaks with lower retention volume, indicating oligomerised/aggregated protein, could be observed.

FIG. 19 SEC analysis of recombinantly expressed, affinity purified Fab-scTRAILR2-SNSN.

SEC analysis of Fab-scTRAILR2-SNSN on a Superdex200 column using PBS, pH 7.4. The diagram shows

the absorption at 280 nm (mAU) plotted against the elution volume (ml). The protein elutes as a distinct peak with an elution volume of 14.12 ml, corresponding to an apparent MW of 87 kDa. No additional protein peaks with lower retention volume, indicating oligomerised/aggregated protein, could be observed.

FIG. 20 SEC analysis of recombinantly expressed, affinity purified Fab-scTRAILwt-SNSN.

SEC analysis of Fab-scTRAILwt-SNSN on a Superdex200 column using PBS, pH 7.4. The diagram shows the absorption at 280 nm (mAU) plotted against the elution volume (ml). The protein elutes as a distinct peak with an elution volume of 13.99 ml, corresponding to an apparent MW of 94 kDa. A small additional protein peak at 12.00 ml could be observed. The apparent Mw of this peak corresponds to about 270 kDa, indicating a defined trimerisation of Fab-scTRAILwt-SNSN. The total protein amount of the peak at 12.00 ml accounts for <3% of the total protein. More than 97% of the analysed Fab-scTRAILwt-SNSN has a defined soluble state (correct assembly of the three receptor binding modules). The peak at 16.12 ml corresponding to a MW of 28 kDa contains Fab-light-chain polypeptide and was not included for the analysis of peak areas.

FIG. 21 Human scTRAIL Linker glycosylation

A: Amino acid sequence of the linker(s) used to combine the receptor binding modules of single chain TRAIL constructs. Gly281 encodes the last amino acid of a respective receptor binding module, the sequence GSGN/SGN/SGS (SEQ ID NOs: 52-54) encodes the linker sequence, Arg121 encodes the first amino acid of the following TRAIL receptor binding domain. The designed linker sequences contains two putative N-linked glycosylation sites at position 1 or 2 as indicated. These positions were permuted as indicated (version I, II, III, SEQ ID NOs: 52-54).

B: Combination of linker positions: The scTRAIL molecules contain three homologue modules (grey barrels) that are connected with linker 1 (SEQ ID NOs: 52-54) and linker 2 (SEQ ID NOs: 52-54) as indicated. Each of the two linkers, can be designed for N-linked glycosylation as described in "A". A complete set of 9 different proteins containing all possible combinations of linkers can be designed based on the sequences shown in B for linker 1 and 2. (Six of these proteins were expressed—see "C").

C: Nomenclature of scTRAIL constructs expressed to test the influence of different linker sequences on glycosylation

FIG. 22 Western Blot analysis of recombinant scTRAIL constructs

Single chain TRAIL proteins with different linker sequences were recombinantly expressed, separated by SDS-PAGE and transferred to a PVDF-membrane. Bound proteins were detected with a mouse monoclonal antibody recognising the Strep-Tag followed by a Peroxidase-conjugated secondary anti-mouse antibody. Different TRAIL variants were loaded as indicated. Note the MW-shift indicating differential glycosylation of scTRAIL-linker variants.

FIG. 23 Cell culture supernatant of HEK293 cells, transiently expressing scCD95L (SEQ ID NO:27) was collected and used to stimulate Jurkat cells at varying concentrations. The supernatant was used either directly without further modifications or an anti-Streptag antibody (2 microgram/ml) was added to cross-link the scCD95L protein. Jurkat cells were incubated with HEK293 cell culture supernatant for

three hours at 37°, lysed and analysed for caspase activity. Only cell supernatant that contained cross-linked scCD95L-St increased caspase activity in Jurkat cells, indicating that scCD95L alone does not form higher order aggregates able to be pro-apoptotic.

FIG. 24 The protein scCD95L (SEQ ID NO:27) can be produced by transient transfection of HEK293 cells, stable transfection of other eukaryotic cells or by expression using prokaryotic cells. The recombinant protein can be affinity purified by using StrepTactin Sepharose matrix. Bound protein can be eluted with a buffer containing desthiobiotin. FIG. 2 shows a silver stained SDS-PAGE of the elution fractions (lanes 1 to 5; fraction 2 is positive) of the affinity purification. The elution fraction containing scCD95L could be applied to size exclusion chromatography (SEC). It is expected, that the protein shows only a low aggregate content.

FIG. 25 Cell culture supernatants of HEK293 cells, transiently expressing single chain TRAIL proteins with different linkers (derived from SEQ ID NO: 28) were collected and used to stimulate Jurkat cells at varying dilutions (exemplarily, a dilution of 1:8 is shown in this figure). The supernatants were used either directly without further modifications or an anti-Streptag antibody (2 microgram/ml Strep MAB Immo) was added to cross-link the scTRAIL proteins. Jurkat cells were incubated with HEK293 cell culture supernatant for three hours at 37°, lysed and analysed for caspase activity. Cell culture supernatant that contained cross-linked scTRAILwt proteins induced an increased caspase activity in Jurkat cells, indicating that scTRAILwt proteins alone do form only a low amount of higher order aggregates able to be pro-apoptotic.

FIG. 26 Influence of the module succession of scTRAIL-construct components on their expression rate of Fab-sc-TRAIL fusion proteins. Western blot of HEK293T cell culture supernatants from transient expression experiments. The polypeptide chains necessary for the formation of the Fab-scTRAIL proteins were either expressed separately (lanes 1 to 10) or alternatively co-expression experiments were performed (lanes 11-13). After reducing SDS-PAGE, proteins were transferred to a nitrocellulose membrane and proteins containing a Streptag were detected, using an anti-Streptag specific mAB as primary AB. The light-chain-scTRAIL(R2-specific) proteins were secreted even in the absence of the accessory heavy chain (lanes 1-4). In contrast, the heavy-chain-scTRAIL(R2-specific) fusion proteins were not secreted in the absence of the accessory light chain (lanes 5-8). As exemplified in lane 13, the heavy-chain-scTRAIL(R2-specific) fusion proteins were only secreted in the presence of the light chain.

FIG. 27 Cell culture supernatants of HEK293T cells, transiently expressing scTRAILwt-Fc fusion proteins with different linkers were collected and used to stimulate Jurkat cells at varying dilutions. The supernatants were used directly without further modifications (Figure XX-A). Jurkat cells were incubated with HEK293T cell culture supernatant for three hours at 37°, lysed and analysed for caspase activity. There was already a pronounced proapoptotic capacity present in the scTRAILwt-Fc containing supernatants, indicating that scTRAILwt-Fc fusion proteins alone do form dimeric assemblies able to be pro-apoptotic.

FIG. 28 A-B It is well known that the use of artificially cross-linked or a membrane-bound ligand of the TNF superfamily has superior bioactivity as compared to soluble, homotrimeric ligand. Thus the local enrichment of single chain TRAIL (scTRAIL) constructs on cells that express the antigen Her2 via the Her2-selective Fab-fragment ("Pertuzumab") fused to these scTRAIL proteins should increase

their cytotoxic bioactivity. Likewise, the blocking of the Her2 binding sites on cells by pre-incubation with the Her2-specific Fab-fragment (Pertuzumab-Fab) only should decrease the cytotoxic bioactivity of Fab-scTRAIL fusion proteins. As shown in A, scTRAIL constructs induce the death of HT1080 cells, as the viability decreases with increasing protein concentration. In accordance, the pre-incubation of HT1080 cells with the Fab-fragment (Pertuzumab-Fab), followed by co-incubation with the Fab-scTRAIL constructs (Fab-sc-TRAILR2-SNSN or Fab-scTRAILwt-SNSN) over night, reduced the cytotoxic activity of the Fab-scTRAIL constructs (B), whereas the Fab only induced no cell death (Pertuzumab-Fab). This means that the Fab-scTRAIL constructs bind to HT1080 cells via the Fab fragment thus increasing the cytotoxic bioactivity of scTRAIL.

DETAILED DESCRIPTION OF THE INVENTION

According to the present invention a substantially non-aggregating fusion polypeptide comprising at least three soluble TNF family ligand domains connected by two peptide linkers is provided.

The term "non-aggregating" refers to a monomer content of the preparation of $\geq 50\%$, preferably $\geq 70\%$ and more preferably $\geq 90\%$. The ratio of monomer content to aggregate content may be determined by examining the amount of aggregate formation using size-exclusion chromatography (SEC). The stability concerning aggregation may be determined by SEC after defined time periods, e.g. from a few to several days, to weeks and months under different storage conditions, e.g. at 4° C. or 25° C. For the fusion protein, in order to be classified as substantially non-aggregating, it is preferred that the monomer content is as defined above after a time period of several days, e.g. 10 days, more preferably after several weeks, e.g. 2, 3 or 4 weeks, and most preferably after several months, e.g. 2 or 3 months of storage at 4° C., or 25° C.

As an increase of e.g. the apoptosis inducing potential in the case of scCD95L on human Jurkat cells correlates with its aggregation state, the stability of the fusion polypeptide concerning aggregation may also be determined by examining the biological activity of the fusion polypeptide.

The single-chain fusion polypeptide may comprise additional domains which may be located at the N- and/or C-termini thereof. Examples for additional fusion domains are e.g. single-chain antibodies or antibody fragments or other targeting molecules or a further cytokine domain, e.g. an interleukin.

The single-chain fusion protein comprises three soluble domains derived from a cytokine of the TNF superfamily. Preferably, those soluble domains are derived from a mammalian, particularly human cytokine including allelic variants and/or derivatives thereof. The soluble domains comprise the extracellular portion of a TNFSF cytokine including the receptor binding domain without membrane located domains. Proteins of the TNF superfamily are anchored to the membrane via an N-terminal portion of 15-30 amino acids, the so-called stalk-region. The stalk region contributes to trimerisation and provides a certain distance to the cell membrane. However, the stalk region is not part of the receptor binding domain (RBD).

Importantly, the RBD is characterised by a particular localisation of its N- and C-terminal amino acids. Said amino acids are immediately adjacent and are located centrally to the axis of the trimer. The first N-terminal amino acids of the RBD form an anti-parallel beta-strand with the C-terminal amino acids of the RBD (FIGS. 2 and 3).

Thus, the anti-parallel beta-strand of the RBD forms an interface with the cell membrane, which is connected to and anchored within the cell membrane via the amino acids of the stalk region. It is highly preferred that the soluble domains of the single-chain fusion protein comprises a receptor binding domain of the TNF-SF cytokine lacking any amino acids from the stalk region (FIGS. 4 and 5). Otherwise, a long linker connecting the C-terminus of one of the soluble domains with the N-terminus of the next soluble domain would be required to compensate for the N-terminal stalk-region of the next soluble domain (FIG. 6), which might result in instability and/or formation of aggregates.

A further advantage of such soluble domains is that the N- and C-terminal amino acids of the RBD are not accessible for any anti-drug antibodies.

Preferably, the single-chain fusion polypeptide is capable of forming an ordered trimeric structure comprising at least one functional binding site for the respective cytokine receptor.

The fusion polypeptide may comprise one, two or three functional cytokine receptor binding sites, i.e. amino acid sequences capable of forming a complex with a cytokine receptor. Thus, at least one of the soluble domains is capable of binding to the corresponding cytokine receptor. In one embodiment, at least one of the soluble domains is capable of receptor activation, whereby apoptotic and/or proliferative activity may be effected. In a further embodiment, one or more of the soluble domains are selected as not being capable of receptor activation.

The soluble domain may be derived from TNF superfamily members, e.g. human TNFSF-1 to -18 and EDA-A1 to -A2 as indicated in Table 1, preferably from LTA (SEQ ID NO:1), TNF α (SEQ ID NO:2), LTB (SEQ ID NO:3), OX40L (SEQ ID NO:4), CD40L (SEQ ID NO:5), CD95L (SEQ ID NO:6), CD27L (SEQ ID NO:7), CD30L (SEQ ID NO:8), CD137L (SEQ ID NO:9), TRAIL (SEQ ID NO:10), RANKL (SEQ ID NO:11), TWEAK (SEQ ID NO:12), APRIL 1 (SEQ ID NO:13), APRIL 2 (SEQ ID NO:14), BAFF (SEQ ID NO:15), LIGHT (SEQ ID NO:16), TL1A (SEQ ID NO:17), GITRL (SEQ ID NO:18), EDA-A1 (SEQ ID NO:19) and EDA-A2 (SEQ ID NO:20). Preferred soluble domains of the respective proteins are indicated in Table 1 (NH₂-aa to COOH-aa) and, e.g., comprise amino acids 59-205, 60-205 or 64-205 of LTA (SEQ ID NO:1), 86-233 of TNF α (SEQ ID NO:2), 82-244 or 86-244 of LTB (SEQ ID NO:3), 52-183 or 55-183 of OX40L (SEQ ID NO:4), 112-261, 117-261 or 121-261 of CD40L (SEQ ID NO:5), 51-193 or 56-193 of CD27L (SEQ ID NO:7), 97-234, 98-234 or 102-234 of CD30L (SEQ ID NO:8), 86-254 of CD137L (SEQ ID NO:9), 161-317 of RANKL (SEQ ID NO:11), 103-249, 104-249, 105-249 or 106-249 of TWEAK (SEQ ID NO:12), 112-247 of APRIL 1 (SEQ ID NO:13), 112-250 of APRIL 2 (SEQ ID NO:14), 140-285 of BAFF (SEQ ID NO:15), 91-251, 93-251 or 97-251 of TL1A (SEQ ID NO:17), 52-177 of GITRL (SEQ ID NO:18), 245-391 of EDA-A1 (SEQ ID NO:19), 245-389 of EDA-A2 (SEQ ID NO:20).

More preferably, the soluble domains are derived from CD95L, TRAIL or LIGHT. In an especially preferred embodiment, the soluble domains are selected from human CD95L, particularly starting from amino acids 144, 145 or 146 and comprise particularly amino acids 144-281 or 145-281 or 146-281 of SEQ ID NO:6 or human TRAIL, particularly starting from amino acids 120-122 and comprise particularly amino acids 120-281, 121-281 or 122-281 of SEQ ID NO:10. Optionally, amino acid Lys145 of SEQ ID NO:6 may be replaced by a non-charged amino acid, e.g. Ser or Gly. Optionally, amino acid Arg121 of SEQ ID NO:10 may be

replaced by a non-charged amino acid, e.g. Ser or Gly. In a further preferred embodiment, the soluble domains are selected from human LIGHT, particularly starting from amino acids 93, 94 or 95 of SEQ ID NO:16 and particularly comprise amino acids 93-240, 94-240 or 95-240 of SEQ ID NO:16.

As indicated above, the soluble domains may comprise the wild-type sequences as indicated in SEQ ID NO: 1-20. It should be noted, however, that it is possible to introduce mutations in one or more of these soluble domains, e.g. mutations which alter (e.g. increase or decrease) the binding properties of the soluble domains. In one embodiment, soluble domains may be selected which cannot bind to the corresponding cytokine receptor. An example of such a mutation is 10 a replacement of amino acid Y218 in human CD95L (SEQ ID NO:6) by another amino acid, e.g. R, K, S or D. Further, a mutation may be introduced which alters the binding to other cellular and/or extracellular components, e.g. the extracellular matrix. An example of such a mutation is a replacement of 15 amino acid K177 in CD95L (SEQ ID NO: 6) by another amino acid, e.g. E, D or S.

In a further preferred embodiment of the invention, the soluble cytokine domain (i) comprises a mutant of the cytokine of the TNF superfamily or a receptor binding domain 20 thereof which binds and/or activates TRAIL-receptor 1 (TRAILR1) and/or TRAIL-receptor 2 (TRAILR2). The binding and/or activity of the mutant may be, e.g., determined by the assays as described in van der Sloot et al. (PNAS, 2006, 103:8634-8639), Kelley et al. (J. Biol. Chem., 2005, 280: 2205-2215), or MacFarlane et al. (Cancer Res., 2005, 65: 30 11265-11270).

The mutant may be generated by any technique and is known by the skilled person, e.g., the techniques described in van der Sloot et al. (PNAS, 2006, 103:8634-8639), Kelley et al. (J. Biol. Chem., 2005, 280:2205-2215), or MacFarlane et al. (Cancer Res., 2005, 65: 11265-11270) and may comprise any type of structural mutations, e.g., substitution, deletion, duplication and/or insertion of an amino acid. A preferred embodiment is the generation of substitutions. The substitution 35 may affect at least one amino acid of the cytokine of the TNF superfamily or a receptor binding domain thereof as described herein. In a preferred embodiment, the substitution may affect at least one of the amino acids of TRAIL, e.g., human TRAIL (e.g., SEQ ID NO: 10). Preferred substitutions 40 in this regard affect at least one of the following amino acids of human TRAIL of SEQ ID NO:10: R130, G160, Y189, R191, Q193, E195, N199, K201, Y213, T214, S215, H264, I266, D267, D269. Preferred amino acid substitutions of 45 human TRAIL of SEQ ID NO:10 are at least one of the following substitutions: R130E, G160M, Y189A, Y189Q, R191K, Q193S, Q193R, E195R, N199V, N199R, K201R, Y213W, T214R, S215D, H264R, I266L, D267Q, D269H, D269R, or D269K.

The amino acid substitution(s) may affect the binding and/or activity of TRAIL, e.g., human TRAIL, to or on either the TRAILR1 or the TRAILR2. Alternatively, the amino acid substitution(s) may affect the binding and/or activity of TRAIL, e.g., human TRAIL, to or on both, the TRAILR1 and the TRAILR2. The binding and/or activity of the TRAILR1 and/or TRAILR2 may be affected positively, i.e., stronger, more selective or more specific binding and/or more activation of the receptor. Alternatively, the binding and/or activity of the TRAILR1 and/or TRAILR2 may be affected negatively, i.e., weaker, less selective or less specific binding and/or less or no activation of the receptor.

Examples of mutants of TRAIL with amino acid substitution(s) of the invention that affect binding and/or activation of

both TRAILR1 and TRAILR2 may be found, e.g., in Table 1 of MacFarlane et al. (cf. above) and may comprise a human TRAIL mutant with the following two amino acid substitutions of SEQ ID NO: 10 Y213W and S215D or with the following single amino acid substitution: Y189A.

Examples of mutants of TRAIL with amino acid substitution(s) of the invention that affect binding and/or activation of TRAILR1 may be found, e.g., in Table 1 of MacFarlane et al. (cf. above) and may comprise a human TRAIL mutant with the following four amino acid substitutions of SEQ ID NO: 10 N199V, K201R, Y213W and S215D or with the following five amino acid substitutions: Q193S, N199V, K201R, Y213W and S215D, or may be found in Table 2 of Kelley et al. (cf. above) and may comprise a human TRAIL mutant with the following six amino acid substitutions: Y213W, S215D, Y189A, Q193S, N199V, and K201R, or with Y213W, S215D, Y189A, Q193S, N199R, and K201R.

Examples of mutants of TRAIL with amino acid substitution(s) of the invention that affect binding and/or activation of TRAILR2 may be found, e.g., in Table 1 of MacFarlane et al. (cf. above) or in Table 2 of Kelley et al. (cf. above) and may comprise a human TRAIL mutant with the following six amino acid substitutions of SEQ ID NO: 10: Y189Q, R191K, Q193R, H264R, I266L, and D267Q, or may be found in Table 2 of van der Sloot et al. (cf. above) and may comprise a human TRAIL mutant with the following single amino acid substitution: D269H, or with the following two amino acid substitutions: D269H and E195R or D269H and T214R.

Thus one preferred embodiment is a fusion protein as described herein wherein at least one of the soluble domains comprises a mutant of TRAIL or of a receptor binding domain thereof which binds and/or activates TRAILR1 and/or TRAILR2.

Further examples of mutants of TRAIL, which show reduced TRAIL induced receptor aggregation are H168 (S, T, Q), R170 (E, S, T, Q) and H177 (S, T).

One preferred embodiment of a fusion protein comprising a mutant of TRAIL or of a receptor binding domain as described herein is a fusion protein wherein component (i) comprises at least one amino acid substitution, particularly as indicated below.

Such an amino acid substitution affects at least one of the following amino acid positions of human TRAIL (SEQ ID NO: 10): R130, G160, H168, R170, H177, Y189, R191, Q193, E195, N199, K201, Y213, T214, S215, H264, I266, D267, D269.

Such an amino acid substitution is at least one of the following: R130E, G160M, H168 (S, T, Q), R170 (E, S, T, Q), H177 (S,T), Y189A, Y189Q, R191K, Q193S, Q193R, E195R, N199V, N199R, K201R, Y213W, T214R, S215D, H264R, I266L, D267Q, D269H, D269R, or D269K.

A preferred TRAIL-R2 selective domain comprises amino acid substitutions Y189Q, R191K, Q193R, H264R, I266L and D267Q.

A preferred TRAIL-R1 selective domain comprises amino acid substitutions Y189A, Q193S, N199V, K201R, Y213W and S215D.

The single-chain fusion molecule of the present invention comprises additionally three soluble cytokine domains, namely components (i), (iii) and (v). According to the present invention, it was surprisingly found that the stability of a single-chain TNF family cytokine fusion polypeptide against aggregation is enhanced, if the second and/or third soluble TNF family cytokine domain is an N-terminally shortened domain which optionally comprises amino acid sequence mutations. Thus, preferably, both the second and the third soluble TNF family cytokine domain are N-terminally short-

ened domains which optionally comprise amino acid sequence mutations in the N-terminal regions, preferably within the first five amino acids of the N-terminus of the soluble cytokine domain. These mutations may comprise replacement of charged, e.g. acidic or basic amino acids, by neutral amino acids, particularly serine or glycine.

In contrast thereto, the selection of the first soluble TNF family cytokine domain is not as critical. Here, a soluble domain having a full-length N-terminal sequence may be used. It should be noted, however, that also the first soluble cytokine domain may have an N-terminally shortened and optionally mutated sequence.

In a preferred embodiment of the present invention, the soluble TNF family cytokine domains (i), (iii) and (v) are soluble CD95L domains, particularly soluble human CD95L domains. The first soluble CD95L domain (i) may be selected from native, shortened and/or mutated sequences. The N-terminal sequence of the first domain (i) may e.g. start between amino acid Glu142 and Val146 of human CD95L, wherein Arg144 and/or Lys145 may be replaced by a neutral amino acid, e.g. by Ser or Gly. The second and third soluble CD95L domains (iii) and (v), however, are selected from shortened and/or mutated sequences. Preferably, at least one of the soluble CD95L domains, (iii) and (v), has an N-terminal sequence which starts between amino acid Arg144 and Val146 of human CD95L, and wherein Arg144 and/or Lys145 may be replaced by a neutral amino acid, e.g. by Ser and/or Gly. In an especially preferred embodiment, the second and third soluble CD95L domain start with an N-terminal sequence selected from:

- (a) Arg144-(Gly/Ser) 145-Val (146)
- (b) (Gly/Ser) 144-Lys145-Val (146) and
- (c) (Gly/Ser) 144-(Gly/Ser) 145-Val (146).

Further, it is preferred that the CD95L domain ends with amino acid Leu 281 of human CD95L.

The soluble CD95L domain may comprise a mammalian, e.g. a human wild-type sequence. In certain embodiments, however, the CD95L sequence may comprise a mutation which results in a reduction or complete inhibition of the binding to the extracellular matrix, e.g. a mutation at position Lys177, e.g. Lys177→Glu, Asp or Ser and/or a mutation which reduces and/or inhibits binding to the CD95L receptor, e.g. a mutation at position Tyr218, e.g. Tyr218→Arg, Lys, Ser, Asp. In certain embodiments of the present invention, one of the three soluble CD95L modules is a sequence variant with a reduced receptor binding. In other embodiments, two of the modules contain mutations resulting in reduced receptor binding.

In a further preferred embodiment of the present invention, the soluble TNF family cytokine domains (i), (iii) and (v) are soluble TRAIL domains, particularly soluble human TRAIL domains. The first soluble TRAIL domain (i) may be selected from native, shortened and/or mutated sequences. Thus, the first soluble TRAIL domain (i) has an N-terminal sequence which may start between amino acid Glu116 and Val122 of human TRAIL, and wherein Arg121 may be replaced by a neutral amino acid, e.g. by Ser or Gly. The second and third soluble TRAIL domains (iii) and (v) have a shortened N-terminal sequence which preferably starts between amino acid Gly120 and Val122 of human TRAIL and wherein Arg121 may be replaced by another amino acid, e.g. Ser or Gly.

Preferably, the N-terminal sequence of the soluble TRAIL

- domains (iii) and (v) is selected from:
- (a) Arg121-Val122-Ala123 and
 - (b) (Gly/Ser)121.

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The soluble TRAIL domain preferably ends with amino acid Gly281 of human TRAIL. In certain embodiments, the TRAIL domain may comprise internal mutations as described above.

In a further preferred embodiment of the present invention, the soluble TNF family cytokine domains (i), (iii) and (v) are soluble LIGHT domains, particularly soluble human LIGHT domains. The first soluble LIGHT domain (i) may be selected from native, shortened and/or mutated sequences. Thus, the first soluble LIGHT domain (i) has an N-terminal sequence which may start between amino acid Glu91 and Ala95 of human LIGHT. The second and third soluble LIGHT domains (iii) and (v) have a shortened N-terminal sequence which preferably starts between amino acid Pro94 and Ala95 of human LIGHT. The soluble LIGHT domain preferably ends with amino acid Val240.

Components (ii) and (iv) of the single-chain fusion polypeptide are peptide linker elements located between components (i) and (iii) or (iii) and (v), respectively. The flexible linker elements have a length of 3-8 amino acids, particularly a length of 3, 4, 5, 6, 7, or 8 amino acids. The linker elements are preferably glycine/serine linkers, i.e. peptide linkers substantially consisting of the amino acids glycine and serine. In cases in which the soluble cytokine domain terminates with S or G (C-terminus), e.g. human TRAIL, the linker starts after S or G. In cases in which the soluble cytokine domain starts with S or G (N-terminus), the linker ends before this S or G.

It should be noted that linker (ii) and linker (iv) do not need to be of the same length. In order to decrease potential immunogenicity, it may be preferred to use shorter linkers. In addition it turned out that shorter linkers lead to single chain molecules with reduced tendency to form aggregates. Whereas linkers that are substantially longer than the ones disclosed here may exhibit unfavourable aggregations properties.

If desired, the linker may comprise an asparagine residue which may form a glycosylation site Asn-Xaa-Ser. In certain embodiments, one of the linkers, e.g. linker (ii) or linker (iv) comprises a glycosylation site. In other embodiments, both linkers (iv) comprise glycosylation sites. In order to increase the solubility of the scTNF-SF proteins and/or in order to reduce the potential immunogenicity, it may be preferred that linker (ii) or linker (iv) or both comprise a glycosylation site.

Preferred linker sequences are selected from GSGSGSGS (SEQ ID NO:52), GSGSGNGS (SEQ ID NO:53), GGSGSGSG (SEQ ID NO:21), GGSGSG (SEQ ID NO:22), GGSG (SEQ ID NO:23), GGSGNGSG (SEQ ID NO:24), GGNGSGSG (SEQ ID NO:25) and GGNGSG (SEQ ID NO:26).

The fusion protein may additionally comprise an N-terminal signal peptide domain, which allows processing, e.g. extracellular secretion, in a suitable host cell. Preferably, the N-terminal signal peptide domain comprises a protease cleavage site, e.g. a signal peptidase cleavage site and thus may be removed after or during expression to obtain the mature protein. Further, the fusion protein may additionally comprise a C-terminal element, having a length of e.g. 1-50, preferably 10-30 amino acids which may include or connect to a recognition/purification domain, e.g. a FLAG domain, a Strep-tag or Strep-tag II domain and/or a poly-His domain.

Further, the fusion polypeptide may additionally comprise N-terminally and/or C-terminally a further domain, e.g. a targeting domain such as a single-chain antibody or an antibody fragment domain. Specific examples of suitable antibodies are anti-tumour antibodies, such as antibodies against

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EGFR-family members. Suitable examples of other targeting molecules are cytokines, such as interleukins.

Examples of specific fusion proteins of the invention are SEQ ID NOs: 27, 28, 29, 43, 45, 47, 49 and 51.

5 A further aspect of the present invention relates to a nucleic acid molecule encoding a fusion protein as described herein. The nucleic acid molecule may be a DNA molecule, e.g. a double-stranded or single-stranded DNA molecule, or an RNA molecule. The nucleic acid molecule may encode the 10 fusion protein or a precursor thereof, e.g. a pro- or pre-pro-form of the fusion protein which may comprise a signal sequence or other heterologous amino acid portions for secretion or purification which are preferably located at the N- and/or C-terminus of the fusion protein. The heterologous 15 amino acid portions may be linked to the first and/or second domain via a protease cleavage site, e.g. a Factor X_a, thrombin or IgA protease cleavage site.

Examples of specific nucleic acid sequences of the invention are SEQ ID NOs: 30, 31 32, 44, 46, 48 and 50.

20 The nucleic acid molecule may be operatively linked to an expression control sequence, e.g. an expression control sequence which allows expression of the nucleic acid molecule in a desired host cell. The nucleic acid molecule may be located on a vector, e.g. a plasmid, a bacteriophage, a viral 25 vector, a chromosomal integration vector, etc. Examples of suitable expression control sequences and vectors are described for example by Sambrook et al. (1989) *Molecular Cloning, A Laboratory Manual*, Cold Spring Harbor Press, and Ausubel et al. (1989), *Current Protocols in Molecular Biology*, John Wiley & Sons or more recent editions thereof.

30 Various expression vector/host cell systems may be used to express the nucleic acid sequences encoding the fusion proteins of the present invention. Suitable host cells include, but are not limited to, prokaryotic cells such as bacteria, e.g. *E. coli*, eukaryotic host cells such as yeast cells, insect cells, plant cells or animal cells, preferably mammalian cells and, more preferably, human cells.

35 Further, the invention relates to a non-human organism transformed or transfected with a nucleic acid molecule as described above. Such transgenic organisms may be generated by known methods of genetic transfer including homologous recombination.

40 A further aspect of the present invention relates to a pharmaceutical or diagnostic composition comprising as the active agent at least one fusion protein, a respective nucleic acid encoding therefore, or a transformed or transfected cell, all as described herein.

45 At least one fusion protein, respective nucleic acid encoding therefore, or transformed or transfected cell, all as described herein may be used in therapy, e.g., in the prophylaxis and/or treatment of disorders caused by, associated with and/or accompanied by dysfunction of TNF-SF cytokines, particularly proliferative disorders, such as tumours, e.g. solid or lymphatic tumours; infectious diseases; inflammatory diseases; metabolic diseases; autoimmune disorders, e.g. rheumatoid and/or arthritic diseases; degenerative diseases, e.g. neurodegenerative diseases such as multiple sclerosis; apoptosis-associated diseases or transplant rejections.

50 The term "dysfunction of TNF-SF cytokines" as used herein is to be understood as any function or expression of a TNF-SF cytokine that deviates from the normal function or expression of a TNF-SF cytokine, e.g., overexpression of the TNF-SF gene or protein, reduced or abolished expression of the TNF-SF cytokine gene or protein compared to the normal 55 physiological expression level of said TNF-SF cytokine, increased activity of the TNF-SF cytokine, reduced or abolished activity of the TNF-SF cytokine, increased binding of

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the TNF-SF cytokine to any binding partners, e.g., to a receptor, particularly a CD95 or TRAIL receptor or another cytokine molecule, reduced or abolished binding to any binding partner, e.g. to a receptor, particularly a CD95 or TRAIL receptor or another cytokine molecule, compared to the normal physiological activity or binding of said TNF-SF cytokine.

The composition may be administered as monotherapy or as combination therapy with further medications, e.g. cytostatic or chemotherapeutic agents, corticosteroids and/or antibiotics.

The fusion protein is administered to a subject in need thereof, particularly a human patient, in a sufficient dose for the treatment of the specific conditions by suitable means. For example, the fusion protein may be formulated as a pharmaceutical composition together with pharmaceutically acceptable carriers, diluents and/or adjuvants. Therapeutic efficacy and toxicity may be determined according to standard protocols. The pharmaceutical composition may be administered systemically, e.g. intraperitoneally, intramuscularly or intravenously or locally, e.g. intranasally, subcutaneously or intrathecally. Preferred is intravenous administration.

The dose of the fusion protein administered will of course be dependent on the subject to be treated, on the subject's weight, the type and severity of the disease, the manner of administration and the judgement of the prescribing physician. For the administration of fusion proteins, a daily dose of 0.001 to 100 mg/kg is suitable.

EXAMPLES

1. Manufacture of a Single-Chain CD95L Fusion Protein (scCD95L)

In the following, the general structure of the recombinant proteins of the invention (FIG. 1) is shown exemplified for the receptor binding domain of the human CD95 ligand.

1.1 Polypeptide Structure

A) Amino Acids Met1-Ser21

IgKappa-signal peptide, assumed signal peptidase cleavage site after amino acid Gly20

B) Amino Acids Glu22-Leu161

First soluble cytokine domain of the human CD95 ligand (CD95L; amino acids 142-281 of SEQ ID NO: 6 including a K145S mutation).

C) Amino Acids Gly162-Gly169

First peptide linker element.

D) Amino Acids Arg170-Leu307

Second soluble cytokine domain of the human CD95 ligand (CD95L; amino acids 144-182 of SEQ ID NO: 6 including a K145S mutation).

E) Amino Acids Gly308-315

Second peptide linker element.

F) Amino Acids Arg316-Leu453

Third soluble cytokine domain of the human CD95 ligand (CD95L; amino acids 144-281 of SEQ ID NO: 6 including a K145S mutation).

G) Amino Acid Gly457-Lys472

Peptide linker with a Strep-tag II motif.

The amino acid sequence of sc CD95L is shown in SEQ ID NO: 27. The fusion polypeptide comprises first and second peptide linkers having the sequence GGSGSGSG (SEQ ID NO: 21). Further preferred linker sequences are SEQ ID NOs: 22-26 as described above. It should be noted that the first and second peptide linker sequences need not to be identical.

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The signal peptide sequence (A) may be replaced by any other suitable, e.g. mammalian signal peptide sequence. The Strep-tag II motif (G) may be replaced by other motifs, if desired, or deleted.

As shown in FIG. 23, cell culture supernatant of HEK293 cells, transiently expressing scCD95L (SEQ ID NO:27) was collected and used to stimulate Jurkat cells at varying concentrations. The supernatant was used either directly without further modifications or an anti-Streptag antibody (2 microgram/ml) was added to cross-link the scCD95L protein. Only cell supernatant that contained cross-linked scCD95L-St increased caspase activity in Jurkat cells, indicating that scCD95L alone does not form higher order aggregates able to be pro-apoptotic.

15 1.2 Gene Cassette Encoding the Polypeptide

The synthetic gene may be optimised in view of its codon-usage for the expression in suitable host cells, e.g. insect cells or mammalian cells. A preferred nucleic acid sequence is shown in SEQ ID NO: 30.

20 1.3 Cloning Strategy

The synthetic gene may be cloned, e.g. by means of a restriction enzyme hydrolysis into a suitable expression vector.

25 2. Manufacture of a Single-Chain TRAIL Fusion Protein (Sc TRAIL Wt)

2.1 Polypeptide Structure

A) Amino Acids Met1-Gly20

30 Ig-Kappa-signal peptide, assumed signal peptidase cleavage site after amino acid Gly 20.

B) Amino Acids Gln21-Gly182

First soluble cytokine domain of the human TRAIL ligand (TRAIL, amino acid 120-281 of SEQ ID NO:10)

35 C) Amino Acids Gly183-Ser 190

First peptide linker element, wherein the two amino acids designated X are both S or one is S and the other one is N.

D) Amino Acids Arg191-Gly351

40 Second soluble cytokine domain of the human TRAIL ligand (TRAIL, amino acids 121-281 of SEQ ID NO:10)

E) Amino Acids Gly 352-Ser359

Second peptide linker element wherein the two amino acids designated X are both S or one is S and the other one is N.

F) Amino Acids Arg360-Gly520

45 Third soluble cytokine domain of the human TRAIL ligand (TRAIL, amino acids 121-Gly281 of SEQ ID NO:10).

G) Amino Acids Gly521-Lys538

50 Peptide linker element with a Streptag II motif.

The amino acid sequence of sc TRAIL wt is shown in SEQ ID NO: 28.

55 The indicated linkers may be replaced by other preferred linkers, e.g. as shown in SEQ ID NOs: 21-26. It should be noted that the first and second peptide linkers do not need to be identical.

60 The signal peptide sequence (A) may be replaced by any other suitable, e.g. mammalian signal peptide sequence. The Strep-tag II motif (G) may be replaced by other motifs, if desired, or deleted.

Cell culture supernatants of HEK293 cells, transiently expressing single chain TRAIL proteins with different linkers (derived from SEQ ID 28, in total nine different linker combinations) were collected and used to stimulate Jurkat cells at varying dilutions (exemplarily, a dilution of 1:8 is shown in FIG. 25). The supernatants were used either directly without further modifications or an anti-Streptag antibody (2 micro-

gram/ml Strep MAB Immo) was added to cross-link the scTRAILwt proteins. Jurkat cells were incubated with HEK293 cell culture supernatant for three hours at 37°, lysed and analysed for caspase activity. Cell culture supernatant that contained cross-linked scTRAILwt proteins induced an increased caspase activity in Jurkat cells (results shown on the right hand side of the graph), indicating that scTRAILwt proteins alone do form only a low amount of higher order aggregates able to be pro-apoptotic.

2.2 Gene Cassette Encoding the Polypeptide

The synthetic gene may be optimised in view of its codon usage for the expression in suitable host cells, e.g. insect cells or mammalian cells. A preferred nucleic acid sequence is shown in SEQ ID NO: 31.

3. Manufacture of a Single-Chain Mutated TRAIL Fusion Protein (scTRAIL (R2-Specific))

In the following, the structure of a single-chain TRAIL polypeptide comprising a mutation for selective binding to TRAIL receptor R2 is shown.

3.1 Polypeptide Structure

A) Amino Acids Met1-Ser29

Ig-Kappa signal peptide, assumed signal peptidase cleavage site after amino acid Gly20 and peptide linker

B) Amino Acids Arg29-Gly190

First soluble cytokine domain of the human TRAIL ligand (TRAIL, amino acids 121-281 of SEQ ID NO: 10 including the mutations Y189Q, R191K, Q193R, H264R, I266L and D267Q)

C) Amino Acid Gly191-Ser198

First peptide linker element, wherein the amino acids designated X are as indicated in Example 2

D) Amino Acids Arg199-Gly359

Second soluble cytokine domain of the human TRAIL ligand (TRAIL amino acids 121-281 of SEQ ID NO: 10 including the mutations as indicated in B)

E) Amino Acids Gly360-Ser367

Second peptide linker element, wherein the amino acids X are as indicated in Example 2

F) Amino Acids Arg368-Gly528

Third soluble cytokine domain of the human TRAIL ligand (TRAIL, amino acids 121-281 of SEQ ID NO: 10 including the mutations as indicated in B)

G) Amino Acids Gly529-Lys546

Peptide linker with a Strep-tag II motif

The amino acid sequence of scTRAIL(R2-specific) is shown in SEQ ID NO: 29.

The indicated linkers may be replaced by other preferred linkers, e.g. as shown in SEQ ID NOs: 21-26. It should be noted that the first and second peptide linkers do not need to be identical.

The signal peptide sequence (A) may be replaced by any other suitable, e.g. mammalian signal peptide sequence. The Strep-tag II motif (G) may be replaced by other motifs, if desired, or deleted.

3.2 Gene Cassette Encoding the Polypeptide

The synthetic gene may be optimised in view of its codon usage for the expression in suitable host cells, e.g. insect cells or mammalian cells. A preferred nucleic acid sequence is shown in SEQ ID NO: 32.

4. Expression and Purification

a) Cloning, Expression and Purification of Fusion Polypeptides

Hek293T cells grown in DMEM+GlutaMAX (GibCo) supplemented with 10% FBS, 100 units/ml Penicillin and 100 µg/ml Streptomycin were transiently transfected with a plasmid containing an expression cassette for a fusion polypep-

tide. In those cases, where a plurality of polypeptide chains is necessary to achieve the final product, e.g. for the Fab-scTNF-SF fusion proteins (FIG. 9A), the expression cassettes were either combined on one plasmid or positioned on different plasmids during the transfection. Cell culture supernatant containing recombinant fusion polypeptide was harvested three days post transfection and clarified by centrifugation at 300×g followed by filtration through a 0.22 µm sterile filter. For affinity purification Streptactin

10 Sepharose was packed to a column (gel bed 1 ml), equilibrated with 15 ml buffer W (100 mM Tris-HCl, 150 mM NaCl, pH 8.0) or PBS pH 7.4 and the cell culture supernatant was applied to the column with a flow rate of 4 ml/min. Subsequently, the column was washed with 15 ml buffer W and bound polypeptide was eluted stepwise by addition of 7×1 ml buffer E (100 mM Tris HCl, 150 mM NaCl, 2.5 mM Desthiobiotin, pH 8.0). Alternately, PBS pH 7.4 containing 2.5 mM Desthiobiotin can be used for this step. The protein amount of the eluate fractions was quantitated and peak fractions were concentrated by ultrafiltration and further purified by size exclusion chromatography (SEC).

15 SEC was performed on a Superdex 200 column using an Äkta chromatography system (GE-Healthcare). The column was equilibrated with phosphate buffered saline and the concentrated, Streptactin-purified polypeptide was loaded onto the SEC column at a flow rate of 0.5 ml/min. The elution profile of the polypeptide was monitored by absorbance at 280 nm. For determination of the apparent molecular weight of purified fusion polypeptide under native conditions a Superdex 200 column was loaded with standard proteins of known molecular weight. Based on the elution volume of the standard proteins a calibration curve was plotted and the apparent molecular weight of purified fusion polypeptide was determined.

5. Apoptosis Assay

35 A cellular assay with a Jurkat A3 permanent T-cell line was used to determine the apoptosis inducing activity of different CD95-ligand (CD95L) and TRAIL fusion polypeptide constructs. Jurkat cells were grown in flasks with RPMI 1640-medium+GlutaMAX (GibCo) supplemented with 10% FBS, 100 units/ml Penicillin and 100 µg/ml Streptomycin. Prior to the assay, 100,000 cells were seeded per well into a 96-well microtiterplate. The addition of different concentrations of fusion peptides to the wells was followed by a 3 hour incubation at 37° C. Cells were lysed by adding lysis buffer (250 mM HEPES, 50 mM MgCl₂, 10 mM EGTA, 5% Triton-X-100, 100 mM DTT, 10 mM AEBSF, pH 7.5) and plates were put on ice for 30 minutes to 2 hours. Apoptosis is paralleled by an increased activity of caspases, e.g. Caspase-3. Hence, cleavage of the specific caspase substrate Ac-DEVD-AFC (Biomol) was used to determine the extent of apoptosis. In fact, Caspase activity correlates with the percentage of apoptotic cells determined morphologically after staining the 45 cells with propidium iodide and Hoechst-33342. For the caspase activity assay, 20 µl cell lysate was transferred to a black 96-well microtiter plate. After the addition of 80 µl buffer containing 50 mM HEPES, 1% Sucrose, 0.1% CHAPS, 50 µM Ac-DEVD-AFC, and 25 mM DTT, pH 7.5, 50 the plate was transferred to a Tecan Infinite 500 microtiter plate reader and the increase in fluorescence intensity was monitored (excitation wavelength 400 nm, emission wavelength 505 nm).

5.1 Cell Death Assay

55 For the determination of cell death in HT1080 fibrosarcoma cells 15,000 cells were plated in 96-well plates over night in RPMI 1640-medium+GlutaMAX (GibCo) supple-

mented with 10% FBS (Biochrom). Cells were coincubated with cycloheximide (Sigma) at a final concentration of 2.5 µg/ml. Cell death was quantified by staining with buffer KV (0.5% crystal violet, 20% methanol). After staining, the wells were washed with water and air-dried. The dye was eluted with methanol and optical density at 595 nm was measured with an ELISA reader.

6. Stability/Aggregation Test

6.1. Principle of the Aggregation Analysis (Definition for Soluble Protein)

The content of monomers (defined trimeric assembly of TNF-SF receptor binding modules) and aggregates is determined by analytical SEC as described in Example 4. For this particular purpose the analysis is performed in buffers containing physiological salt concentrations at physiological pH (e.g. 0.9% NaCl, pH 7.4; PBS pH 7.4). A typical aggregation analysis is done on a Superdex200 column (GE Healthcare). This column separates proteins in the range between 10 to 800 kDa.

For determination of the apparent molecular weight of purified fusion polypeptide under native conditions a Superdex 200 column is loaded with standard proteins of known molecular weight. Based on the elution volume of the standard proteins a calibration curve is plotted and the apparent molecular weight of purified fusion polypeptide is calculated based on the elution volume.

SEC analysis of soluble, non aggregated proteins,—e.g. trimeric TNF-SF, typically shows a distinct single protein peak at a defined elution volume. This elution volume corresponds to the apparent native molecular weight of the particular protein and approximately complies to the theoretical molecular weight calculated on the basis of the primary amino acid sequence.

If protein aggregation occurs the SEC analysis shows additional protein peaks with lower retention volumes. For TNF-SF family members the aggregation of soluble proteins occurs in a characteristic manner. The proteins tend to form oligomers of the “trimers”, forming nonamers (3x3) and 27mers (3x9). These oligomers serve as aggregation seeds and a high content of oligomers potentially leads to aggregation of the protein. Oligomers of large molecular weight and aggregates elute in the void volume of the Superdex200 column and cannot be analysed by SEC with respect to their native molecular weight. Examples for SEC analysis of a defined soluble trimeric and a oligomerised/aggregated preparation of TNF-SF proteins are shown in FIG. 17.

Due to the induction of (complete) aggregation, purified preparations of TNF-SF fusion proteins should preferably contain only defined trimeric proteins and only a very low amount of oligomerised protein.

The degree of aggregation/oligomerisation of a particular TNF-SF protein preparation is determined on basis of the SEC analysis by calculating the peak areas of the OD280 diagram for the defined trimeric and the oligomer/aggregate fraction, respectively. Based on the total peak area the percentage of defined trimeric protein is calculated as follows:

$$\text{(% Trimer content)} = \frac{\text{[Peak area trimer]}}{\text{[Total peak area]}} \times 100$$

The definition for soluble protein as used in this text, describes a protein preparation of purified TNF-SF protein in a buffer of physiological salt concentrations at physiological pH that contains a defined soluble protein (trimeric assembly of TNF-SF domains) content of >90% within a typical protein concentration range from 0.2 to 10.0 mg/ml.

6.2 SEC Aggregation Analysis for Purified Sc-TRAIL Variants

Three different sc-TRAIL variants were transfected and affinity purified as described. The purified proteins were subsequently analysed for their content of defined soluble protein using SEC analysis as described in 6.1. In the particular case of single chain fusion proteins a trimer describes a trimeric assembly of three encoded TNF-SF domains encoded by a single polypeptide chain. (Formally single chain TNF-SF proteins are monomers, since single chain assemblies do only form intramolecular interactions [all protein domains are encoded by a single polypeptide chain] and do not form intermolecular interactions between distinct individual polypeptide chains.)

- 15 The proteins analysed by SEC were:
 - 1.) Fab-Sc-TRAIL(R2-Specific)-SNSN (FIG. 19): Fusion protein comprising an Fab domain fused N-terminal to a single chain fusion protein of TRAIL specific for TRAIL-receptor 2 interaction, glycosylated
 - 2.) Fab-Sc-TRAIL(R2-Specific)-SSSS (FIG. 18): Fusion protein comprising an Fab domain fused N-terminal to a single chain fusion protein of TRAIL specific for TRAIL-receptor 2 interaction, non glycosylated
 - 3.) Fab-Sc-TRAIL-Wt-SNSN (FIG. 20): Fusion protein comprising an Fab domain fused N-terminal to a single chain TRAIL, glycosylated

The SEC analysis for the three purified Fab-sc-constructs of TRAIL revealed a single protein peak for all proteins indicating defined soluble protein fractions (>95% trimer). The calculated apparent MW for the proteins (based on calibration of the column) strongly indicate a trimeric association of the TNF-SF-domains for the purified proteins. None of the analysed proteins showed indications for aggregation (FIGS. 18, 19, 20).

Comparing the potentially glycosylated “Fab-sc-TRAIL-R2-SNSN” with the non glycosylated “Fab-sc-TRAIL-R2-SSSS” indicates a significant difference of the apparent native MW that is due to glycosylation of Fab-sc-TRAIL(R2-specific)-SNSN.

40 Expression of sc-TNF-SF members as fusion protein with an antibody fv-fragment is known to facilitate aggregation of the protein. The construction principle of the Fab-sc-TRAIL variants revealed no aggregation of the expressed TRAIL variants and is therefore beneficial with respect to solubility of the protein.

6.3 Differential Glycosylation of Sc-TRAIL-Linker Variants

Glycosylation of proteins can be beneficial for recombinant sc-TNF-SF constructs with regard to potential immunogenicity and stability. In order to get glycosylation of the sc-TRAIL construct, specific linker sequences were designed that contained putative N-linked glycosylation sites at defined positions (see FIG. 21-A). Recombinant expression and subsequent Western-Blot analysis revealed that the respective position of the Asparagine (N) within the linker sequence is important for the subsequent glycosylation of the protein. Surprisingly, the preferential linker position of the glycosylated asparagine was identified to be at position “2” as described in FIG. 21-A, (G S G S G N G S). If the asparagine is localised at other positions (e.g. position “1” [G S G N G S G S] see FIG. 21-A), glycosylation of the respective asparagine(s) is abolished. This aspect could be confirmed by Western-Blot analysis of different sc-TRAIL variants. If both asparagines of linker 1 and linker 2 were localised at position “2” a significant glycosylation dependant MW-shift could be observed for the respective sc-TRAIL variant (FIG. 22). A MW-shift of the glycosylated sc-TRAIL linker variant could also be confirmed by calculating the apparent MW after

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SEC analysis (FIG. 18, 19). The non-glycosylated Fab-sc-TRAIL(R2-specific)SSSS has a clearly lower MW (68 kDa) compared to glycosylated Fab-sc-TRAIL(R2-specific)SNSN (87 kDa).

Based on this analysis we claim differential glycosylation of the sc-TRAIL constructs by modifying the position of the asparagines within the linker sequence(s). Glycosylation protects the linker sequence towards proteolytic degradation and might stabilise the protein. In addition glycosylation of the linker sequence potentially prevents recognition of the linker sequence by the immune system and potentially reduces the immunogenicity of the protein. Therefore glycosylation of the linker sequence is beneficial with regard to immunogenicity and proteolytic stability of the sc-TRAIL constructs and has potential influence on the half life of the protein. The linker specific differential glycosylation can be used to modify the immunogenicity and stability of recombinant TNF-SF members.

6.3. Expression and Analysis of a Sc-TRAIL with Prolonged Linker Sequence and N-Terminal Stalk Residues (Sc-TRAIL-(95-281)-Long)

In WO/2005/103077 a single chain TRAIL-fusion polypeptide, herein named sc-TRAIL-(95-281)-long, is described, wherein each TRAIL module comprise residues 95 to 281 of SEQ ID NO:10. The TRAIL modules are linked by Glycine Serine linker comprising of at least 12 amino acids (GGGSGGGGSGGGGS). Compared to the TRAIL modules of the present invention (comprising residues 121-281 of SEQ ID NO:10), additional 25 amino acids including the stalk region are present in each of the adjacent TRAIL modules.

In order to analyse the influence of the linker sequence on sc-TRAIL constructs, sc-TRAIL-(95-281)-long is analysed. Expression, purification and subsequent SEC analysis reveals that sc-TRAIL-(95-281)-long with the 12 aa linker and the additional stalk sequence is expressed and secreted to the cell culture supernatant of HEK293T cells. However, SEC analysis of the purified protein indicates that sc-TRAIL-(95-281)-long shows multiple peaks comprising a large amount of protein in an oligomerised or aggregated form. Aggregation of sc-TRAIL-(95-281)-long is a direct effect of the prolonged linker sequences in combination with the additional residues of the N-terminal stalk. The results indicate that the longer linker used in this construct leads to increased aggregation properties of the construct.

7. Construction of Single-Chain Fusion Polypeptides Comprising One or More Additional Domains

7.1. Assembly of Soluble TNF-SF and Antibody Fragments Known from the Art

It is known from the art that soluble TNF-SF cytokine domains may be fused to antibody fragments in order to obtain trimerisation and/or dimerization of trimers. Single-chain scFv-TNF-SF fusion proteins have been constructed consisting of a single-chain antibody and a soluble domain comprising a TNF-RBD and the stalk-region. The corresponding trimers consist of three single-chain antibodies and three soluble domains (FIG. 7).

In addition, Fc-TNF-SF fusion proteins, wherein each fusion protein comprises an N-terminal intramolecular Fc-domain and a C-terminal soluble domain have been constructed (FIG. 8). The dimerization of soluble domains is accomplished by assembly of two Fc-domains via disulfide bridges. Trimers are subsequently obtained by a combination of two soluble domains from one Fc-TNF-SF fusion protein and one soluble domain from another Fc-TNF-SF fusion protein. As can be deduced from FIG. 4, dimerization of

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trimers is also mediated by the N-terminal Fc-TNF-SF fusion. In conclusion, three Fc-antibody fragments are present per dimer of the trimer. However, such fusion proteins are likely to form higher molecular weight aggregates, which represents a major disadvantage.

7.2. Fusion Proteins of the Invention Comprising One or More Additional Domains

The inventive fusion proteins comprising one or more additional domains can be constructed in several ways. In the following, the construction of fusion proteins with additional domains is exemplified with the antibody pertuzumab directed against the cell surface antigen ErbB2. The amino acid sequence of the heavy chain is shown in SEQ ID NO: 33:

1 EVOLVESGGG LVQPGGSLRL SCAASGFTFT DYTMDWVRQA
PGKGLEWVAD VNPNSGGSIY
61 NQRFKGRFTL SVDRSKNTLY LQMNSLRAED TAVYYCARNL
GPSFYFDYWG QGTLTVSSA
121 STKGPSVFP APSSKSTSGG TAALGCLVKD YFPEPVTVSW
NSGALTSGVH TFPAVLQSSG
181 LYSLSSVVTV PSSSLGTQTY ICNVNHKPSN TKVDKKVEPK SC

The amino acid sequence of the light chain is shown in SEQ ID NO: 34

30 1 DIQMTQSPSS LSASVGDRVT ITCKASQDVS IGVAWYQQKP
GKAPKLIIYS ASYRYTGVP
61 RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YYIYPYTFGQ
GTKVEIKRTV AAPSVFIFPP
121 SDEQLKSGTA SVVCLLNPFY PREAKVQWKV DNAHQSGNSQ
ESVTEQDSKD STYSLSSTLT
181 LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGECA

7.2.1

40 In one embodiment, the fusion polypeptide of the invention further comprises an N- or C-terminal Fab-antibody fragment (FIG. 9A).

The fusion of an antibody Fab-fragment to the N-terminus of scTNF-SF fusion polypeptide may be accomplished by the following two strategies:

(i) The heavy chain sequence is extended by further amino acids from the IgG1 hinge region and fused to the single-chain TNF-SF fusion protein.

50 The IgG1 hinge region comprises the amino acid sequence SEQ ID NO: 35:

. . . KSC₁DKTHTC₂PPC₃LPAPE . . .

55 In a preferred embodiment, the Fab-domain is chosen such that the C-terminal cysteine of the heavy chain (C1 of the hinge region) terminates the CH1 domain. This cysteine is required for forming a disulfide linkage to the light chain.

60 The subsequent linker comprises portions of the IgG hinge region (e.g. DKTHT or DKT), however without further cysteines of the hinge region. Alternatively, a glycine-serine linker is used. Due to the absence of further cysteines, a monomeric fusion protein comprising two polypeptide chains is obtained. The linker preferably has a length of 3-15 amino acids. More preferably, the linker is selected from the linker 1-7 as shown below.

SEQ ID NOS: 55-56
1. DKTHTG(S)a(G)b; (a = 0-5; b = 0 or 1),
SEQ ID NOS: 57-61
2. DKTHTGS(S)a(GS)bG(S)c (a, b = 0, 1-6; c = 0 or 1),
SEQ ID NO: 62
3. DKTG(S)a(G)b; (a = 0-5; b = 0 or 1),
SEQ ID NOS: 63-67 10
4. DKTG(S)a(GS)bG(S)c (a, b = 0, 1-6; c = 0 or 1),
SEQ ID NOS: 68-69
5. SSG(S)a(GS)bG(S)c (a, b = 0, 1-6; c = 0 or 1),
SEQ ID NO: 71 15
6. SS(GGGS)aG(S)b (a = 0, 1-4; b = 0 or 1),
SEQ ID NO: 72
7. GSPGSSSSS(G)a (a = 0 or 1),

Preferred amino acid sequences with the heavy chain module positioned N-terminal to the scTNF-SF module are shown in SEQ ID NO: 45, SEQ ID NO: 47 and SEQ ID NO: 49. For production purposes, these polypeptide chains are coexpressed with the Fab light chain polypeptide (SEQ ID NO: 40) to finally achieve the Fab-scTRAIL fusion polypeptides.

(ii) The light-chain sequence is fused to the single chain TNF-SF fusion protein.

The constant region of the light chain (e.g. SEQ ID NO: 34) ends with a C-terminal cysteine residue. This residue may be covalently bridged with the C1 hinge cysteine of the heavy chain.

Preferably, the linkers 1-7 as shown below are used for the connection between the light chain sequence and the TNF-SF fusion protein. Linkers 5-7 are preferred (see above).

Preferably, the last amino acid in the linker adjacent to the cytokine module is either Gly or Ser. In the following, preferred linker sequences are shown:

Further, the linker may comprise N-glycosylation motifs (NXS/T, wherein X may be any amino acid).

One embodiment of the amino acid sequences with the light chain module positioned N-terminal to the scTNF-SF module is shown in SEQ ID NO: 51.

In the case of the Fab-scTNF-SF fusion proteins, the co-expression of two polypeptide chains is necessary to achieve the correct assembly of the Fab module in addition to the scTNF-SF module (see FIG. 9A). The Pertuzumab heavy and light chain modules (SEQ ID NO: 33 and SEQ ID NO: 34) were equipped with a signal peptide, back translated and the resulting synthetic genes (SEQ ID NO: 41 and SEQ ID NO: 42) genetically fused upstream of the scTRAILwt- or scTRAILR2-specific gene modules (SEQ ID NO: 31 and SEQ ID NO: 32). Examples for the resulting gene cassettes are shown in SEQ ID NO: 46, 48 and 50. After subcloning into appropriate expression vectors, a selection of the resulting plasmids was used for transient protein expression in HEK293T cells. The heavy chain TRAIL or light chain TRAIL expression plasmids were transfected either alone or in combination with the necessary light or heavy chain encoding vectors of the Fab-Fragment (FIG. 26). Surprisingly, the module combination within the fusion proteins influenced the relative stability of the scTRAIL-protein during secretory based expression. If the light-chain module of the Fab-domain is fused N-terminal to the scTRAIL-domain (exemplified in SEQ ID NO: 51), the expression product is stable itself and secreted, when expressed separately (Lanes 1-4, FIG. 26). It can be therefore expected, when such a fusion polypep-

tide is coexpressed with a heavy-chain module, that two major protein species will be formed during a potential production process: (1) the Fab-scTRAIL fusion protein consisting of two polypeptide chains and (2) as contamination a light-chain-scTRAIL fusion protein without a functional Fab domain. Therefore, fusing the heavy-chain module N-terminal to the scTNF-SF-module for the expression is preferred to avoid this technical disadvantage.

A functional analysis of recombinant inventive Fab comprising-scTRAIL fusion proteins with the heavy-chain module fused N-terminal to the scTRAIL-module (Fab-scTRAILR2-SNSN or Fab-scTRAILwt-SNSN) is shown in FIG. 28. As final purification step, size exclusion chromatography was employed as exemplified in FIGS. 19 and 20.

Superior bioactivity compared to soluble, homotrimeric ligands can easily be achieved by the use of artificially cross-linked or a membrane-bound ligand of the TNF superfamily. Thus the local enrichment of single chain TRAIL (scTRAIL) constructs on cells that express the antigen Her2 via the Her2-selective Fab-fragment ("Pertuzumab") fused to these scTRAIL proteins should increase their cytotoxic bioactivity. Likewise, the blocking of the Her2 binding sites on cells by pre-incubation with the Her2-specific Fab-fragment (Pertuzumab-Fab) only should decrease the cytotoxic bioactivity of Fab-scTRAIL fusion proteins. As shown in FIG. 28A, scTRAIL constructs induce the death of HT1080 cells, as the viability decreases with increasing protein concentration. In accordance, the pre-incubation of HT1080 cells with the Fab-fragment (Pertuzumab-Fab), followed by co-incubation with the Fab-scTRAIL constructs (Fab-scTRAILR2-SNSN or Fab-scTRAILwt-SNSN) over night, reduced the cytotoxic activity of the Fab-scTRAIL constructs (FIG. 28B), whereas the Fab only induced no cell death.

An increased technical effect may be achieved by use of artificially cross-linked or a membrane-bound ligands of the TNF superfamily resulting especially in superior bioactivity as compared to soluble, homotrimeric ligand. Thus the local enrichment of ligands or single chain ligands such as exemplified by single chain TRAIL (scTRAIL) on cells or on neighbouring cells should increase the bioactivity of these fusion proteins. The local enrichment (or targeting) of these single chain ligands can be specifically induced for instance by fusing the single chain ligands with amino acid sequences that bind to any antigen present on cells such as for instance tumor cells. Examples for antigen binding sequences may be derived from antibodies such as scFv or Fab fragments. Examples for antigens expressed on target cells may be receptors such as from the EGFR family or any other antigen to which a binding antibody can be generated. Of special interest in this context are cell surface antigens specific for tumor or cancer cells.

7.2.2

In another embodiment, the fusion polypeptide of the invention further comprises an additional N- or C-terminal scFv-antibody fragment (FIG. 9B).

In this embodiment linkers 5-7 as described above may be used. Further, the linkers may comprise N-glycosylation motifs.

A preferred single chain Fv-pertuzumab fragment for fusing to the single-chain cytokine fusion protein may comprise amino acids Glu1-Ser119 of SEQ ID NO: 33 and Asp-Lys107 or Thr109 of SEQ ID NO: 34. The VH and VL fragments may be connected by a linker.

One embodiment of a scFv-domain of pertuzumab is shown in the following SEQ ID NO: 36:

1 METDTLLLWV LLLWVPAGNG EVQLVESGGG LVQPGGSLRL
SCAASGFTFT DYTMDWVRQA

61 PGKGLEWWAD VNPNSGGSIY NQRFKGRFTL SVDRSKNTLY
LQMNSLRAED TAVYYCARNL

121 GPSFYFDYWG QGTLTVVSSG GGGSGGGSG GGGSDIQMTO
SPSSLASAVG DRVTITCKAS

181 QDVSIGVAWY QQKPGKAPKL LIYSASYRYT GVPSRFGSG
SGTDFLTIS SLQPEDFATY

241 YCQQQYYIYPY TFGQGTKVEI KRT

Amino acids 1-20 (underlined) constitute an N-terminal secretory signal peptide.

7.2.3

In a further embodiment, the fusion polypeptide of the invention comprises an additional N- or C-terminal Fc-antibody fragment (FIGS. 10 and 11).

Preferably, the Fc-antibody fragment domain is derived from a human immunoglobulin G heavy chain, particularly from a human immunoglobulin IgG1 heavy chain. In an especially preferred embodiment, the amino acid sequence of the Fc-domain is shown in SEQ ID NO: 37.

1 KSCDKTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTP
EVTCVVVDVS HEDPEVKFNW

61 YVDGVEVHNA KTKPREEQYN STYRVSVLT VLHQDWLNGK
EYKCKVSNKA LPAPIEKITIS

121 KAKGQPREPQ VYTLPPSREE MTKNQVSLTC LVKGFPYPSDI
AVEWESNGQP ENNYKTTTPV

181 LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT
QKSLSLSPGK

Amino acids Lys1-Glu16 define the hinge region.

For a C-terminal fusion (FIG. 11) the Fc-domain preferably comprises the complete constant domain (amino acids 17-230 of SEQ ID NO: 37) and a part or the complete hinge region, e.g. the complete hinge region or the hinge region starting from amino acid Asp4.

Preferred linkers for connecting a C-terminal Fc-antibody fragment (e.g. FIG. 11) are shown in the following:

Linker 8 SEQ ID NOS: 73-78
scCD95L/scTRAIL. . .GG(P/S)_a(GS)_b(G/S)_c
KSCDKTHTCPPCPAPE. . .
(a = 0 or 1; b = 0-8; c = 0-8),

Linker 9 SEQ ID NOS: 79-80
scCD95L/scTRAIL. . .GG(P/S)_a(GSSGS)_bGS(G/S)_c
DKTHTCPPCPAPE. . .
(a = 0 or 1; b = 0-8; c = 0-8),

Linker 10 SEQ ID NOS: 81-82
scCD95L/scTRAIL. . .GG(P/S)_a(S)_b(GS)_c(G/S)_d
DKTHTCPPCPAPE. . .
(a = 0 or 1; b = 0-8; c = 0-8; d = 0-8),

All linkers start with GlyGly taking in account, however, that the C-terminal amino acid of TRAIL is a Gly. At position 3 of the linker, alternatively Pro or Ser are present. Linker 8 comprises the Cys1 cysteine of the heavy chain.

It should be noted that linkers 8-10 are also suitable for the C-terminal fusion of other polypeptides, e.g. a further scTNF-SF fusion protein.

In detail, the scTRAILwt module (SEQ ID NO: 28), the scTRAIL(R2-specific)-module (SEQ ID NO: 29) and the

scCD95L-module (SEQ ID NO: 27) were fused N-terminally to the Fc-domain of human IgG1, starting with Asp4 of SEQ ID NO: 37 employing four linker elements as shown in Table 1.

5

TABLE 1

Sequences linking the Fc-domain C-terminally to scTNF-SF module.		
Fc-Fusion	Amino-acid sequence of the linker element	
FC01	. . .(G)GSPGSSSSSSGSDKTH. . .	SEQ ID NO: 97
FC02	. . .(G)GSPGSSSSGS <u>D</u> KTH. . .	SEQ ID NO: 98
FC03	. . .(G)GSPGSSG <u>S</u> DKTH. . .	SEQ ID NO: 99
FC04	. . .(G)GSSDKTH. . .	SEQ ID NO: 100

The N-terminal amino-acid of the IgG1 CH2-domain is underlined. The N-terminal Glycine of the linking sequence is shown in brackets. For TNF-SF proteins with a glycine as the C-terminal amino acid (e.g. TRAIL), the N-terminal glycine of the linking sequence formally belongs to the scTNF-SF module.

For purification and characterisation, a Strep-tag II (amino acid sequence WSHPQFEK, SEQ ID NO: 102) was placed 25 C-terminally to the Fc-domain. This affinity tag was linked to the CH3-domain by a flexible linker element (amino acid sequence SSSSSSA, SEQ ID NO: 101), replacing the C-terminal lysine residue of the CH3-sequence. The amino acid sequences of the scTNF-SF fusion proteins as well as for the described protein modules were backtranslated and their codon usage was optimised for mammalian cell-based expression. Gene synthesis was done by ENTELECHON GmbH (Regensburg, Germany). The expression cassettes for larger fusion proteins were assembled by common cloning 30 procedures starting with DNA-modules of suitable size and suitable restriction enzyme pattern. Exemplarily, the resulting gene cassette for the single chain TRAILwt FC01 fusion protein (scTRAILwt-FC01) is shown in SEQ ID NO: 44 and the encoded protein sequence is shown in SEQ ID NO: 43. 35 The gene cassettes encoding the shortened linker variants (table 1) were generated by PCR based subcloning strategies, starting from SEQ ID NO: 44. The final expression cassettes were released from intermediate cloning vectors and sub-cloned into to pCDNA4-HisMax-backbone, using unique Hind-III-, Not-I- or Xba-I sites of the plasmid. For the assembly of the Fab- and Fc-fusions proteins, a unique SgS-I site 40 was introduced into the vector backbone, replacing the Not-I-site. All expression cassettes were routinely verified by DNA sequencing. The proteins were transiently expressed in HEK293T cells and the cell culture supernatants were monitored regarding their pro-apoptotic activity. As shown in FIG. 45 50 55 60 65 70 75 80 85 90 95 100 27, the scTRAIL-Fc fusion proteins of the invention, were able to induce a pronounced increase in caspase activity, confirming the potency of the Fc-based dimerization of two scTRAILwt-modules. Similar results were obtained for scTRAIL(R2-specific)-Fc fusion proteins (data not shown). If an Fc-antibody fragment is fused to the N-terminus of an scTNF-SF fusion protein (cf. FIG. 10), the amino acid sequence of the Fc-module is preferably as shown in SEQ ID NO: 38:

1 METDTLLLWV LLLWVPAGNG DKTHTCP
FLFPPKPKDT LMISRTPEVT

61 CVVVDVSHED PEVKFNWYVD GVEVHNKTK PREEQYNSTY
RVVSVLTVLH QDWLNGKEYK

25

-Continued

121 CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSREEMTK
NQVSLTCLVK GFYPSDIAVE

181 WESNGQPENN YKTPPPVLD SGSFFLYSKL TVDKSRWQQG
NWFSCVMHE ALHNHYTQKS

241 LSLSPG

Amino acids 1-20 (underlined) constitute an N-terminal secretory signal peptide.

For connecting the Fc-module to the ScTNF-SF fusion protein, preferably Gly/Ser linkers are used. All linkers preferably start with a serine and preferably end with glycine or serine. Preferred linker sequences 11-12 are shown in the following:

11. $(S)_a(GS)_bG(S)_c$ (a, b=0, 1-6; c=0 or 1), SEQ ID Nos: 15
83-85

12. $S(GGGS)_aG_b(S)_c$ (a, b=0, 1-6; c=0 or 1), SEQ ID NO: 86
7.3 Dimerization of the Single-Chain Fusion Proteins of the Invention

7.3.1 Single-Chain Fusion Polypeptides Comprising One 20 Additional Domain

The trimeric fusion proteins of the invention can further be dimerized.

In one embodiment, dimerization will be obtained if the C-terminus of a first fusion protein is directly connected to the N-terminus of a second fusion protein via a linker structure as defined herein (FIG. 12).

In another embodiment, a fusion protein of the invention comprising an Fab-antibody fragment as an additional domain, may be connected via a linker as defined herein directly with a further fusion protein of the invention or indirectly via an scFv-antibody fragment fused to a further fusion protein of the invention (FIG. 13). Thereby, dimerization of the trimeric fusion proteins of the invention is accomplished.

In another embodiment, dimerization of trimers may be obtained via the assembly of two fusion proteins of the invention comprising a Fab-antibody fragment as an additional domain (FIG. 14). In this case, intermolecular disulfide bridges are formed.

For the construction of dimerizing Fab fragments N-terminal to the scTNF-SF domain (e.g. FIG. 14), preferably the natural cysteine residues of the IgG hinge region (SEQ ID NO: 35) are used.

Preferably the C-terminal cysteine of the Fab-sequence corresponds to the C1-residue of the hinge region, which forms a disulfide bond with the light chain. The second cysteine C2 may be used for the covalent linkage of two Fab-modules. A third cysteine residue C3 may be open or linked with the C3 of the neighbouring chain. Preferred linkers between the Fab heavy chain sequence and the N-terminus of the scTNF-SF domain are linkers 13-22 as shown below.

SEQ ID NO: 87

13. $DKTHTCGPSS(GS)_aG(S)_b$,

26

-Continued

SEQ ID NO: 88

14. $DKTHTCGPSS_aG(S)_b$,

SEQ ID NO: 89

15. $DKTHTC(GSSGS)_aGSG(S)_b$,

SEQ ID NO: 90

16. $DKTHTCGSS(GS)_aG(S)_b$,

SEQ ID NO: 91

17. $DKTHTCGSS_aG(S)_b$,

SEQ ID NO: 92

18. $DKTHTC(GSSGS)_aGS(G)_b$,

SEQ ID NO: 93

19. $DKTHTCPCPGSSGSGSGS$ (G)_b,

SEQ ID NO: 94

20. $DKTHTCPCP(GSSGS)$ _aGS(G)_b,

SEQ ID NO: 95

21. $DKTHTCPCPGSS(GS)$ _aGS(G)_b,

SEQ ID NO: 96

22. $DKTHTCPCPGSS$ _aGS(G)_b,

Further, the linkers may be modified by incorporation of N-glycosylation motifs as described above.

In a further embodiment, dimerization of the fusion proteins of the invention comprising an Fc-antibody fragment as an additional N- and/or C-terminal domain, may be obtained by the formation of intermolecular disulfide bridges between two of said fusion proteins. In that case, only one Fc-antibody fragment is present per dimer of a trimeric fusion protein. Thereby, in contrast to the Fc-antibody fragment fusion proteins of the art, formation of higher molecular weight aggregates is not very likely.

7.3.2 Single-Chain Fusion Polypeptides Comprising a Plurality of Additional Domains

The single-chain fusion polypeptide may comprise one or more additional domains, e.g. a further antibody fragment and/or a further targeting domain and/or a further cytokine domain.

40 A fusion protein of the invention comprising an Fc-antibody fragment as one additional domain may be connected to a further Fab- or scFv-antibody fragment via the N-terminus of an N-terminal fused Fc-antibody fragment (FIG. 15) or directly via its N-terminus through a further linker structure (FIG. 16), if the Fc-antibody fragment is connected to the fusion protein of the invention via its C-terminus.

45 In addition to a further antibody fragment or instead of the further antibody fragment, a further cytokine, preferably an interleukin, may be connected to the fusion protein. Thereby, it is possible to obtain a combination of an agonistic scCD95L and an antagonistic scCD95L molecule or alternatively combinations of scTRAIL (R1-specific) and scTRAIL (R2-specific). Said fusion proteins are especially useful for the induction of apoptosis.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 102

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<210> SEQ ID NO 1
<211> LENGTH: 205
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: human LTA

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27

28

-continued

<400> SEQUENCE: 1

Met Thr Pro Pro Glu Arg Leu Phe Leu Pro Arg Val Cys Gly Thr Thr
 1 5 10 15

Leu His Leu Leu Leu Leu Gly Leu Leu Val Leu Leu Pro Gly Ala
 20 25 30

Gln Gly Leu Pro Gly Val Gly Leu Thr Pro Ser Ala Ala Gln Thr Ala
 35 40 45

Arg Gln His Pro Lys Met His Leu Ala His Ser Thr Leu Lys Pro Ala
 50 55 60

Ala His Leu Ile Gly Asp Pro Ser Lys Gln Asn Ser Leu Leu Trp Arg
 65 70 75 80

Ala Asn Thr Asp Arg Ala Phe Leu Gln Asp Gly Phe Ser Leu Ser Asn
 85 90 95

Asn Ser Leu Leu Val Pro Thr Ser Gly Ile Tyr Phe Val Tyr Ser Gln
 100 105 110

Val Val Phe Ser Gly Lys Ala Tyr Ser Pro Lys Ala Thr Ser Ser Pro
 115 120 125

Leu Tyr Leu Ala His Glu Val Gln Leu Phe Ser Ser Gln Tyr Pro Phe
 130 135 140

His Val Pro Leu Leu Ser Ser Gln Lys Met Val Tyr Pro Gly Leu Gln
 145 150 155 160

Glu Pro Trp Leu His Ser Met Tyr His Gly Ala Ala Phe Gln Leu Thr
 165 170 175

Gln Gly Asp Gln Leu Ser Thr His Thr Asp Gly Ile Pro His Leu Val
 180 185 190

Leu Ser Pro Ser Thr Val Phe Phe Gly Ala Phe Ala Leu
 195 200 205

<210> SEQ ID NO 2

<211> LENGTH: 233

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<223> OTHER INFORMATION: human TNFa

<400> SEQUENCE: 2

Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
 1 5 10 15

Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
 20 25 30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
 35 40 45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
 50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
 65 70 75 80

Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
 85 90 95

Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
 100 105 110

Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
 115 120 125

Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
 130 135 140

-continued

Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
145 150 155 160

Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
165 170 175

Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
180 185 190

Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
195 200 205

Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
210 215 220

Gln Val Tyr Phe Gly Ile Ile Ala Leu
225 230

<210> SEQ_ID NO 3

<211> LENGTH: 244

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<223> OTHER INFORMATION: human LTA

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<223> OTHER INFORMATION: human LTB

<400> SEQUENCE: 3

Met Gly Ala Leu Gly Leu Glu Gly Arg Gly Gly Arg Leu Gln Gly Arg
1 5 10 15

Gly Ser Leu Leu Leu Ala Val Ala Gly Ala Thr Ser Leu Val Thr Leu
20 25 30

Leu Leu Ala Val Pro Ile Thr Val Leu Ala Val Leu Ala Leu Val Pro
35 40 45

Gln Asp Gln Gly Gly Leu Val Thr Glu Thr Ala Asp Pro Gly Ala Gln
50 55 60

Ala Gln Gln Gly Leu Gly Phe Gln Lys Leu Pro Glu Glu Pro Glu
65 70 75 80

Thr Asp Leu Ser Pro Gly Leu Pro Ala Ala His Leu Ile Gly Ala Pro
85 90 95

Leu Lys Gly Gln Gly Leu Gly Trp Glu Thr Thr Lys Glu Gln Ala Phe
100 105 110

Leu Thr Ser Gly Thr Gln Phe Ser Asp Ala Glu Gly Leu Ala Leu Pro
115 120 125

Gln Asp Gly Leu Tyr Tyr Cys Leu Val Gly Tyr Arg Gly Arg
130 135 140

Ala Pro Pro Gly Gly Asp Pro Gln Gly Arg Ser Val Thr Leu Arg
145 150 155 160

Ser Ser Leu Tyr Arg Ala Gly Gly Ala Tyr Gly Pro Gly Thr Pro Glu
165 170 175

Leu Leu Leu Glu Gly Ala Glu Thr Val Thr Pro Val Leu Asp Pro Ala
180 185 190

Arg Arg Gln Gly Tyr Gly Pro Leu Trp Tyr Thr Ser Val Gly Phe Gly
195 200 205

Gly Leu Val Gln Leu Arg Arg Gly Glu Arg Val Tyr Val Asn Ile Ser
210 215 220

His Pro Asp Met Val Asp Phe Ala Arg Gly Lys Thr Phe Phe Gly Ala
225 230 235 240

Val Met Val Gly

-continued

<210> SEQ_ID NO 4
<211> LENGTH: 183
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: human OX40L

<400> SEQUENCE: 4

Met	Glu	Arg	Val	Gln	Pro	Leu	Glu	Glu	Asn	Val	Gly	Asn	Ala	Ala	Arg
1															15
	5						10								
Pro	Arg	Phe	Glu	Arg	Asn	Lys	Leu	Leu	Leu	Val	Ala	Ser	Val	Ile	Gln
								20	25					30	
Gly	Leu	Gly	Leu	Leu	Leu	Cys	Phe	Thr	Tyr	Ile	Cys	Leu	His	Phe	Ser
								35	40			45			
Ala	Leu	Gln	Val	Ser	His	Arg	Tyr	Pro	Arg	Ile	Gln	Ser	Ile	Lys	Val
								50	55			60			
Gln	Phe	Thr	Glu	Tyr	Lys	Lys	Glu	Lys	Gly	Phe	Ile	Leu	Thr	Ser	Gln
					65			70			75				80
Lys	Glu	Asp	Glu	Ile	Met	Lys	Val	Gln	Asn	Asn	Ser	Val	Ile	Ile	Asn
								85	90			95			
Cys	Asp	Gly	Phe	Tyr	Leu	Ile	Ser	Leu	Lys	Gly	Tyr	Phe	Ser	Gln	Glu
					100				105			110			
Val	Asn	Ile	Ser	Leu	His	Tyr	Gln	Lys	Asp	Glu	Glu	Pro	Leu	Phe	Gln
								115	120			125			
Leu	Lys	Lys	Val	Arg	Ser	Val	Asn	Ser	Leu	Met	Val	Ala	Ser	Leu	Thr
								130	135			140			
Tyr	Lys	Asp	Lys	Val	Tyr	Leu	Asn	Val	Thr	Thr	Asp	Asn	Thr	Ser	Leu
					145				150			155			160
Asp	Asp	Phe	His	Val	Asn	Gly	Gly	Glu	Leu	Ile	Leu	Ile	His	Gln	Asn
					165				170			175			
Pro	Gly	Glu	Phe	Cys	Val	Leu									
					180										

<210> SEQ_ID NO 5
<211> LENGTH: 261
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: human CD40L

<400> SEQUENCE: 5

Met	Ile	Glu	Thr	Tyr	Asn	Gln	Thr	Ser	Pro	Arg	Ser	Ala	Ala	Thr	Gly
1															15
	5							10							
Leu	Pro	Ile	Ser	Met	Lys	Ile	Phe	Met	Tyr	Leu	Leu	Thr	Val	Phe	Leu
								20	25			30			
Ile	Thr	Gln	Met	Ile	Gly	Ser	Ala	Leu	Phe	Ala	Val	Tyr	Leu	His	Arg
								35	40			45			
Arg	Leu	Asp	Lys	Ile	Glu	Asp	Glu	Arg	Asn	Leu	His	Glu	Asp	Phe	Val
								50	55			60			
Phe	Met	Lys	Thr	Ile	Gln	Arg	Cys	Asn	Thr	Gly	Glu	Arg	Ser	Leu	Ser
								65	70			75			80
Leu	Leu	Asn	Cys	Glu	Glu	Ile	Lys	Ser	Gln	Phe	Glu	Gly	Phe	Val	Lys
								85	90			95			
Asp	Ile	Met	Leu	Asn	Lys	Glu	Glu	Thr	Lys	Lys	Glu	Asn	Ser	Phe	Glu
								100	105			110			

-continued

Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
115 120 125

Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
130 135 140

Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln
145 150 155 160

Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
165 170 175

Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser
180 185 190

Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
195 200 205

Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His
210 215 220

Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn
225 230 235 240

Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe
245 250 255

Gly Leu Leu Lys Leu
260

<210> SEQ_ID NO 6
<211> LENGTH: 281
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: human CD95L

<400> SEQUENCE: 6

Met Gln Gln Pro Phe Asn Tyr Pro Tyr Pro Gln Ile Tyr Trp Val Asp
1 5 10 15

Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu Pro Cys
20 25 30

Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro Pro Pro
35 40 45

Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Pro Leu Pro
50 55 60

Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly
65 70 75 80

Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly
85 90 95

Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Leu Ala
100 105 110

Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser Leu Glu
115 120 125

Lys Gln Ile Gly His Pro Ser Pro Pro Glu Lys Lys Glu Leu Arg
130 135 140

Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro Leu
145 150 155 160

Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr
165 170 175

Lys Lys Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr
180 185 190

Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro Leu Ser
195 200 205

-continued

His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu Val Met
210 215 220

Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln Met Trp Ala
225 230 235 240

Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His
245 250 255

Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn Phe Glu Glu Ser
260 265 270

Gln Thr Phe Phe Gly Leu Tyr Lys Leu
275 280

<210> SEQ ID NO 7

<211> LENGTH: 193

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<223> OTHER INFORMATION: human CD27L

<400> SEQUENCE: 7

Met Pro Glu Glu Gly Ser Gly Cys Ser Val Arg Arg Arg Pro Tyr Gly
1 5 10 15

Cys Val Leu Arg Ala Ala Leu Val Pro Leu Val Ala Gly Leu Val Ile
20 25 30

Cys Leu Val Val Cys Ile Gln Arg Phe Ala Gln Ala Gln Gln Leu
35 40 45

Pro Leu Glu Ser Leu Gly Trp Asp Val Ala Glu Leu Gln Leu Asn His
50 55 60

Thr Gly Pro Gln Gln Asp Pro Arg Leu Tyr Trp Gln Gly Pro Ala
65 70 75 80

Leu Gly Arg Ser Phe Leu His Gly Pro Glu Leu Asp Lys Gly Gln Leu
85 90 95

Arg Ile His Arg Asp Gly Ile Tyr Met Val His Ile Gln Val Thr Leu
100 105 110

Ala Ile Cys Ser Ser Thr Thr Ala Ser Arg His His Pro Thr Thr Leu
115 120 125

Ala Val Gly Ile Cys Ser Pro Ala Ser Arg Ser Ile Ser Leu Leu Arg
130 135 140

Leu Ser Phe His Gln Gly Cys Thr Ile Ala Ser Gln Arg Leu Thr Pro
145 150 155 160

Leu Ala Arg Gly Asp Thr Leu Cys Thr Asn Leu Thr Gly Thr Leu Leu
165 170 175

Pro Ser Arg Asn Thr Asp Glu Thr Phe Phe Gly Val Gln Trp Val Arg
180 185 190

Pro

<210> SEQ ID NO 8

<211> LENGTH: 234

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<223> OTHER INFORMATION: human CD30L

<400> SEQUENCE: 8

Met Asp Pro Gly Leu Gln Gln Ala Leu Asn Gly Met Ala Pro Pro Gly
1 5 10 15

Asp Thr Ala Met His Val Pro Ala Gly Ser Val Ala Ser His Leu Gly

-continued

20	25	30
Thr Thr Ser Arg Ser Tyr Phe Tyr	Leu Thr Thr Ala Thr	Leu Ala Leu
35	40	45
Cys Leu Val Phe Thr Val Ala Thr Ile Met Val	Leu Val Val Gln Arg	
50	55	60
Thr Asp Ser Ile Pro Asn Ser Pro Asp Asn Val Pro	Leu Lys Gly Gly	
65	70	75
Asn Cys Ser Glu Asp Leu Leu Cys Ile Leu Lys Arg	Ala Pro Phe Lys	
85	90	95
Lys Ser Trp Ala Tyr Leu Gln Val Ala Lys His Leu Asn	Lys Thr Lys	
100	105	110
Leu Ser Trp Asn Lys Asp Gly Ile Leu His Gly Val Arg	Tyr Gln Asp	
115	120	125
Gly Asn Leu Val Ile Gln Phe Pro Gly Leu Tyr Phe Ile	Ile Cys Gln	
130	135	140
Leu Gln Phe Leu Val Gln Cys Pro Asn Asn Ser Val Asp	Leu Lys Leu	
145	150	155
Glu Leu Leu Ile Asn Lys His Ile Lys Lys Gln Ala	Leu Val Thr Val	
165	170	175
Cys Glu Ser Gly Met Gln Thr Lys His Val Tyr Gln Asn	Leu Ser Gln	
180	185	190
Phe Leu Leu Asp Tyr Leu Gln Val Asn Thr Thr Ile Ser	Val Asn Val	
195	200	205
Asp Thr Phe Gln Tyr Ile Asp Thr Ser Thr Phe Pro	Leu Glu Asn Val	
210	215	220
Leu Ser Ile Phe Leu Tyr Ser Asn Ser Asp		
225	230	

<210> SEQ ID NO 9
<211> LENGTH: 254
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: human CD137L

<400> SEQUENCE: 9

Met Glu Tyr Ala Ser Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp Pro
1 5 10 15

Pro Ala Pro Arg Ala Arg Ala Cys Arg Val Leu Pro Trp Ala Leu Val
20 25 30

Ala Gly Leu Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val Phe
35 40 45

Leu Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser
50 55 60

Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp
65 70 75 80

Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val
85 90 95

Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp
100 105 110

Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu
115 120 125

Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe
130 135 140

-continued

Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser
145 150 155 160

Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala
165 170 175

Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala
180 185 190

Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala
195 200 205

Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His
210 215 220

Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val
225 230 235 240

Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
245 250

<210> SEQ ID NO 10
<211> LENGTH: 281
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: human TRAIL

<400> SEQUENCE: 10

Met Ala Met Met Glu Val Gln Gly Gly Pro Ser Leu Gly Gln Thr Cys
1 5 10 15

Val Leu Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys Val Ala
20 25 30

Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys
35 40 45

Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr
50 55 60

Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val
65 70 75 80

Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser
85 90 95

Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro
100 105 110

Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly
115 120 125

Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu
130 135 140

Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly
145 150 155 160

His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile
165 170 175

His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe
180 185 190

Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln
195 200 205

Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys
210 215 220

Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr
225 230 235 240

Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile
245 250 255

-continued

Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala
 260 265 270

Ser Phe Phe Gly Ala Phe Leu Val Gly
 275 280

<210> SEQ_ID NO 11
<211> LENGTH: 317
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: human RANKL

<400> SEQUENCE: 11

Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu
 1 5 10 15

Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His Ala
 20 25 30

Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met
 35 40 45

Phe Val Ala Leu Leu Gly Leu Gly Leu Gln Val Val Cys Ser Val
 50 55 60

Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser
 65 70 75 80

Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn
 85 90 95

Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile
 100 105 110

Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln
 115 120 125

Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys
 130 135 140

Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu
 145 150 155 160

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro
 165 170 175

Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly
 180 185 190

Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val
 195 200 205

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
 210 215 220

His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val
 225 230 235 240

Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met
 245 250 255

Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe
 260 265 270

Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu
 275 280 285

Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
 290 295 300

Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
 305 310 315

-continued

<210> SEQ ID NO 12
<211> LENGTH: 249
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: human TWEAK

<400> SEQUENCE: 12

```

Met Ala Ala Arg Arg Ser Gln Arg Arg Arg Gly Arg Arg Gly Glu Pro
1           5          10          15

Gly Thr Ala Leu Leu Val Pro Leu Ala Leu Gly Leu Gly Leu Ala Leu
20          25          30

Ala Cys Leu Gly Leu Leu Leu Ala Val Val Ser Leu Gly Ser Arg Ala
35          40          45

Ser Leu Ser Ala Gln Glu Pro Ala Gln Glu Glu Leu Val Ala Glu Glu
50          55          60

Asp Gln Asp Pro Ser Glu Leu Asn Pro Gln Thr Glu Glu Ser Gln Asp
65          70          75          80

Pro Ala Pro Phe Leu Asn Arg Leu Val Arg Pro Arg Arg Ser Ala Pro
85          90          95

Lys Gly Arg Lys Thr Arg Ala Arg Ala Ile Ala Ala His Tyr Glu
100         105         110

Val His Pro Arg Pro Gly Gln Asp Gly Ala Gln Ala Gly Val Asp Gly
115         120         125

Thr Val Ser Gly Trp Glu Ala Arg Ile Asn Ser Ser Ser Pro Leu
130         135         140

Arg Tyr Asn Arg Gln Ile Gly Glu Phe Ile Val Thr Arg Ala Gly Leu
145         150         155         160

Tyr Tyr Leu Tyr Cys Gln Val His Phe Asp Glu Gly Lys Ala Val Tyr
165         170         175

Leu Lys Leu Asp Leu Leu Val Asp Gly Val Leu Ala Leu Arg Cys Leu
180         185         190

Glu Glu Phe Ser Ala Thr Ala Ala Ser Ser Leu Gly Pro Gln Leu Arg
195         200         205

Leu Cys Gln Val Ser Gly Leu Leu Ala Leu Arg Pro Gly Ser Ser Leu
210         215         220

Arg Ile Arg Thr Leu Pro Trp Ala His Leu Lys Ala Ala Pro Phe Leu
225         230         235         240

Thr Tyr Phe Gly Leu Phe Gln Val His
245

```

<210> SEQ ID NO 13
<211> LENGTH: 247
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: human APRIL_ver1

<400> SEQUENCE: 13

```

Met Pro Ala Ser Ser Pro Phe Leu Leu Ala Pro Lys Gly Pro Pro Gly
1           5          10          15

Asn Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala Leu Trp
20          25          30

Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala Met Ala Leu
35          40          45

Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu Val Ser Arg

```

-continued

50	55	60
Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly Tyr Pro Trp		
65	70	75
80		
Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala Trp Glu Asn		
85	90	95
Gly Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln Lys Gln Lys		
100	105	110
Lys Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys		
115	120	125
Asp Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg		
130	135	140
Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala		
145	150	155
160		
Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe		
165	170	175
Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr		
180	185	190
Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr		
195	200	205
Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile		
210	215	220
Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro		
225	230	235
240		
His Gly Thr Phe Leu Gly Leu		
245		

<210> SEQ_ID NO 14
<211> LENGTH: 250
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: human APRIL_ver2

<400> SEQUENCE: 14

Met Pro Ala Ser Ser Pro Phe Leu Leu Ala Pro Lys Gly Pro Pro Gly		
1	5	10
15		
Asn Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala Leu Trp		
20	25	30
Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala Met Ala Leu		
35	40	45
Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu Val Ser Arg		
50	55	60
Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly Tyr Pro Trp		
65	70	75
80		
Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala Trp Glu Asn		
85	90	95
Gly Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln Lys Gln Lys		
100	105	110
Lys Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys		
115	120	125
Asp Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg		
130	135	140
Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala		
145	150	155
160		

-continued

Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe
165 170 175

Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr
180 185 190

Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr
195 200 205

Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile
210 215 220

Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro
225 230 235 240

His Gly Thr Phe Leu Gly Phe Val Lys Leu
245 250

<210> SEQ_ID NO 15

<211> LENGTH: 285

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<223> OTHER INFORMATION: human BAFF

<400> SEQUENCE: 15

Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu
1 5 10 15

Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
20 25 30

Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
35 40 45

Ala Ala Thr Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
50 55 60

Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
65 70 75 80

Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
85 90 95

Ala Pro Lys Ala Gly Leu Glu Ala Pro Ala Val Thr Ala Gly Leu
100 105 110

Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
115 120 125

Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
130 135 140

Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
145 150 155 160

Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
165 170 175

Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr
180 185 190

Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
195 200 205

Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
210 215 220

Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu
225 230 235 240

Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly
245 250 255

Asp Glu Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu
260 265 270

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```
Asp Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
275          280          285
```

<210> SEQ ID NO 16
<211> LENGTH: 240
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: human LIGHT

<400> SEQUENCE: 16

```
Met Glu Glu Ser Val Val Arg Pro Ser Val Phe Val Val Asp Gly Gln
1           5           10          15
```

```
Thr Asp Ile Pro Phe Thr Arg Leu Gly Arg Ser His Arg Arg Gln Ser
20          25          30
```

```
Cys Ser Val Ala Arg Val Gly Leu Gly Leu Leu Leu Leu Met Gly
35          40          45
```

```
Ala Gly Leu Ala Val Gln Gly Trp Phe Leu Leu Gln Leu His Trp Arg
50          55          60
```

```
Leu Gly Glu Met Val Thr Arg Leu Pro Asp Gly Pro Ala Gly Ser Trp
65          70          75          80
```

```
Glu Gln Leu Ile Gln Glu Arg Arg Ser His Glu Val Asn Pro Ala Ala
85          90          95
```

```
His Leu Thr Gly Ala Asn Ser Ser Leu Thr Gly Ser Gly Pro Leu
100         105         110
```

```
Leu Trp Glu Thr Gln Leu Gly Leu Ala Phe Leu Arg Gly Leu Ser Tyr
115         120         125
```

```
His Asp Gly Ala Leu Val Val Thr Lys Ala Gly Tyr Tyr Tyr Ile Tyr
130         135         140
```

```
Ser Lys Val Gln Leu Gly Gly Val Gly Cys Pro Leu Gly Leu Ala Ser
145         150         155         160
```

```
Thr Ile Thr His Gly Leu Tyr Lys Arg Thr Pro Arg Tyr Pro Glu Glu
165         170         175
```

```
Leu Glu Leu Leu Val Ser Gln Gln Ser Pro Cys Gly Arg Ala Thr Ser
180         185         190
```

```
Ser Ser Arg Val Trp Trp Asp Ser Ser Phe Leu Gly Gly Val Val His
195         200         205
```

```
Leu Glu Ala Gly Glu Lys Val Val Val Arg Val Leu Asp Glu Arg Leu
210         215         220
```

```
Val Arg Leu Arg Asp Gly Thr Arg Ser Tyr Phe Gly Ala Phe Met Val
225         230         235         240
```

<210> SEQ ID NO 17
<211> LENGTH: 251
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: human TL1A

<400> SEQUENCE: 17

```
Met Ala Glu Asp Leu Gly Leu Ser Phe Gly Glu Thr Ala Ser Val Glu
1           5           10          15
```

```
Met Leu Pro Glu His Gly Ser Cys Arg Pro Lys Ala Arg Ser Ser Ser
20          25          30
```

```
Ala Arg Trp Ala Leu Thr Cys Cys Leu Val Leu Pro Phe Leu Ala
35          40          45
```

-continued

Gly Leu Thr Thr Tyr Leu Leu Val Ser Gln Leu Arg Ala Gln Gly Glu
50 55 60

Ala Cys Val Gln Phe Gln Ala Leu Lys Gly Gln Glu Phe Ala Pro Ser
65 70 75 80

His Gln Gln Val Tyr Ala Pro Leu Arg Ala Asp Gly Asp Lys Pro Arg
85 90 95

Ala His Leu Thr Val Val Arg Gln Thr Pro Thr Gln His Phe Lys Asn
100 105 110

Gln Phe Pro Ala Leu His Trp Glu His Glu Leu Gly Leu Ala Phe Thr
115 120 125

Lys Asn Arg Met Asn Tyr Thr Asn Lys Phe Leu Leu Ile Pro Glu Ser
130 135 140

Gly Asp Tyr Phe Ile Tyr Ser Gln Val Thr Phe Arg Gly Met Thr Ser
145 150 155 160

Glu Cys Ser Glu Ile Arg Gln Ala Gly Arg Pro Asn Lys Pro Asp Ser
165 170 175

Ile Thr Val Val Ile Thr Lys Val Thr Asp Ser Tyr Pro Glu Pro Thr
180 185 190

Gln Leu Leu Met Gly Thr Lys Ser Val Cys Glu Val Gly Ser Asn Trp
195 200 205

Phe Gln Pro Ile Tyr Leu Gly Ala Met Phe Ser Leu Gln Glu Gly Asp
210 215 220

Lys Leu Met Val Asn Val Ser Asp Ile Ser Leu Val Asp Tyr Thr Lys
225 230 235 240

Glu Asp Lys Thr Phe Phe Gly Ala Phe Leu Leu
245 250

<210> SEQ ID NO 18
<211> LENGTH: 177
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: human GITRL

<400> SEQUENCE: 18

Met Cys Leu Ser His Leu Glu Asn Met Pro Leu Ser His Ser Arg Thr
1 5 10 15

Gln Gly Ala Gln Arg Ser Ser Trp Lys Leu Trp Leu Phe Cys Ser Ile
20 25 30

Val Met Leu Leu Phe Leu Cys Ser Phe Ser Trp Leu Ile Phe Ile Phe
35 40 45

Leu Gln Leu Glu Thr Ala Lys Glu Pro Cys Met Ala Lys Phe Gly Pro
50 55 60

Leu Pro Ser Lys Trp Gln Met Ala Ser Ser Glu Pro Pro Cys Val Asn
65 70 75 80

Lys Val Ser Asp Trp Lys Leu Glu Ile Leu Gln Asn Gly Leu Tyr Leu
85 90 95

Ile Tyr Gly Gln Val Ala Pro Asn Ala Asn Tyr Asn Asp Val Ala Pro
100 105 110

Phe Glu Val Arg Leu Tyr Lys Asn Lys Asp Met Ile Gln Thr Leu Thr
115 120 125

Asn Lys Ser Lys Ile Gln Asn Val Gly Gly Thr Tyr Glu Leu His Val
130 135 140

Gly Asp Thr Ile Asp Leu Ile Phe Asn Ser Glu His Gln Val Leu Lys

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145	150	155	160
-----	-----	-----	-----

Asn Asn Thr Tyr Trp Gly Ile Ile Leu Leu Ala Asn Pro Gln Phe Ile			
165	170	175	

Ser

<210> SEQ ID NO 19

<211> LENGTH: 391

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<223> OTHER INFORMATION: human EDA-A1

<400> SEQUENCE: 19

Met Gly Tyr Pro Glu Val Glu Arg Arg Glu Leu Leu Pro Ala Ala Ala			
1	5	10	15

Pro Arg Glu Arg Gly Ser Gln Gly Cys Gly Cys Gly Ala Pro Ala			
20	25	30	

Arg Ala Gly Glu Gly Asn Ser Cys Leu Leu Phe Leu Gly Phe Phe Gly			
35	40	45	

Leu Ser Leu Ala Leu His Leu Leu Thr Leu Cys Cys Tyr Leu Glu Leu			
50	55	60	

Arg Ser Glu Leu Arg Arg Glu Arg Gly Ala Glu Ser Arg Leu Gly Gly			
65	70	75	80

Ser Gly Thr Pro Gly Thr Ser Gly Thr Leu Ser Ser Leu Gly Gly Leu			
85	90	95	

Asp Pro Asp Ser Pro Ile Thr Ser His Leu Gly Gln Pro Ser Pro Lys			
100	105	110	

Gln Gln Pro Leu Glu Pro Gly Glu Ala Ala Leu His Ser Asp Ser Gln			
115	120	125	

Asp Gly His Gln Met Ala Leu Leu Asn Phe Phe Pro Asp Glu Lys			
130	135	140	

Pro Tyr Ser Glu Glu Glu Ser Arg Arg Val Arg Arg Asn Lys Arg Ser			
145	150	155	160

Lys Ser Asn Glu Gly Ala Asp Gly Pro Val Lys Asn Lys Lys Lys Gly			
165	170	175	

Lys Lys Ala Gly Pro Pro Gly Pro Asn Gly Pro Pro Gly Pro Pro Gly			
180	185	190	

Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile Pro Gly Ile Pro Gly Ile			
195	200	205	

Pro Gly Thr Thr Val Met Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly			
210	215	220	

Pro Gln Gly Pro Pro Gly Leu Gln Gly Pro Ser Gly Ala Ala Asp Lys			
225	230	235	240

Ala Gly Thr Arg Glu Asn Gln Pro Ala Val Val His Leu Gln Gly Gln			
245	250	255	

Gly Ser Ala Ile Gln Val Lys Asn Asp Leu Ser Gly Gly Val Leu Asn			
260	265	270	

Asp Trp Ser Arg Ile Thr Met Asn Pro Lys Val Phe Lys Leu His Pro			
275	280	285	

Arg Ser Gly Glu Leu Glu Val Leu Val Asp Gly Thr Tyr Phe Ile Tyr			
290	295	300	

Ser Gln Val Glu Val Tyr Tyr Ile Asn Phe Thr Asp Phe Ala Ser Tyr			
305	310	315	320

Glu Val Val Val Asp Glu Lys Pro Phe Leu Gln Cys Thr Arg Ser Ile

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325	330	335
Glu Thr Gly Lys Thr Asn Tyr Asn Thr Cys Tyr Thr Ala Gly Val Cys 340	345	350
Leu Leu Lys Ala Arg Gln Lys Ile Ala Val Lys Met Val His Ala Asp 355	360	365
Ile Ser Ile Asn Met Ser Lys His Thr Thr Phe Phe Gly Ala Ile Arg 370	375	380
Leu Gly Glu Ala Pro Ala Ser 385	390	
 <210> SEQ_ID NO 20		
<211> LENGTH: 389		
<212> TYPE: PRT		
<213> ORGANISM: Homo sapiens		
<220> FEATURE:		
<221> NAME/KEY: MISC_FEATURE		
<223> OTHER INFORMATION: human EDA-A2		
 <400> SEQUENCE: 20		
Met Gly Tyr Pro Glu Val Glu Arg Arg Glu Leu Leu Pro Ala Ala Ala 1	5	10
Pro Arg Glu Arg Gly Ser Gln Gly Cys Gly Cys Gly Gly Ala Pro Ala 20	25	30
Arg Ala Gly Glu Gly Asn Ser Cys Leu Leu Phe Leu Gly Phe Phe Gly 35	40	45
Leu Ser Leu Ala Leu His Leu Leu Thr Leu Cys Cys Tyr Leu Glu Leu 50	55	60
Arg Ser Glu Leu Arg Arg Glu Arg Gly Ala Glu Ser Arg Leu Gly Gly 65	70	75
Ser Gly Thr Pro Gly Thr Ser Gly Thr Leu Ser Ser Leu Gly Gly Leu 85	90	95
Asp Pro Asp Ser Pro Ile Thr Ser His Leu Gly Gln Pro Ser Pro Lys 100	105	110
Gln Gln Pro Leu Glu Pro Gly Glu Ala Ala Leu His Ser Asp Ser Gln 115	120	125
Asp Gly His Gln Met Ala Leu Leu Asn Phe Phe Phe Pro Asp Glu Lys 130	135	140
Pro Tyr Ser Glu Glu Glu Ser Arg Arg Val Arg Arg Asn Lys Arg Ser 145	150	155
Lys Ser Asn Glu Gly Ala Asp Gly Pro Val Lys Asn Lys Lys Lys Gly 165	170	175
Lys Lys Ala Gly Pro Pro Gly Pro Asn Gly Pro Pro Gly Pro Pro Gly 180	185	190
Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile Pro Gly Ile Pro Gly Ile 195	200	205
Pro Gly Thr Thr Val Met Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly 210	215	220
Pro Gln Gly Pro Pro Gly Leu Gln Gly Pro Ser Gly Ala Ala Asp Lys 225	230	235
Ala Gly Thr Arg Glu Asn Gln Pro Ala Val Val His Leu Gln Gly Gln 245	250	255
Gly Ser Ala Ile Gln Val Lys Asn Asp Leu Ser Gly Gly Val Leu Asn 260	265	270
Asp Trp Ser Arg Ile Thr Met Asn Pro Lys Val Phe Lys Leu His Pro 275	280	285

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Arg Ser Gly Glu Leu Glu Val Leu Val Asp Gly Thr Tyr Phe Ile Tyr
290 295 300

Ser Gln Val Tyr Tyr Ile Asn Phe Thr Asp Phe Ala Ser Tyr Glu Val
305 310 315 320

Val Val Asp Glu Lys Pro Phe Leu Gln Cys Thr Arg Ser Ile Glu Thr
325 330 335

Gly Lys Thr Asn Tyr Asn Thr Cys Tyr Thr Ala Gly Val Cys Leu Leu
340 345 350

Lys Ala Arg Gln Lys Ile Ala Val Lys Met Val His Ala Asp Ile Ser
355 360 365

Ile Asn Met Ser Lys His Thr Thr Phe Phe Gly Ala Ile Arg Leu Gly
370 375 380

Glu Ala Pro Ala Ser
385

<210> SEQ ID NO 21
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: linker

<400> SEQUENCE: 21

Gly Gly Ser Gly Ser Gly Ser Gly
1 5

<210> SEQ ID NO 22
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: linker

<400> SEQUENCE: 22

Gly Gly Ser Gly Ser Gly
1 5

<210> SEQ ID NO 23
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: linker

<400> SEQUENCE: 23

Gly Gly Ser Gly
1

<210> SEQ ID NO 24
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: linker

<400> SEQUENCE: 24

Gly Gly Ser Gly Asn Gly Ser Gly
1 5

<210> SEQ ID NO 25
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

-continued

<223> OTHER INFORMATION: linker

<400> SEQUENCE: 25

Gly Gly Asn Gly Ser Gly Ser Gly
1 5

<210> SEQ ID NO 26

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: linker

<400> SEQUENCE: 26

Gly Gly Asn Gly Ser Gly
1 5

<210> SEQ ID NO 27

<211> LENGTH: 472

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: fusion protein scCD95L

<400> SEQUENCE: 27

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Ala Gly Asn Gly Ser Glu Leu Arg Ser Val Ala His Leu Thr Gly Lys
20 25 30

Ser Asn Ser Arg Ser Met Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile
35 40 45

Val Leu Leu Ser Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn
50 55 60

Glu Thr Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln
65 70 75 80

Ser Cys Asn Asn Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn Ser
85 90 95

Lys Tyr Pro Gln Asp Leu Val Met Met Glu Gly Lys Met Met Ser Tyr
100 105 110

Cys Thr Thr Gly Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val
115 120 125

Phe Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu Leu
130 135 140

Ser Leu Val Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys
145 150 155 160

Leu Gly Gly Ser Gly Ser Gly Arg Ser Val Ala His Leu Thr
165 170 175

Gly Lys Ser Asn Ser Arg Ser Met Pro Leu Glu Trp Glu Asp Thr Tyr
180 185 190

Gly Ile Val Leu Leu Ser Gly Val Lys Tyr Lys Lys Gly Gly Leu Val
195 200 205

Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg
210 215 220

Gly Gln Ser Cys Asn Asn Leu Pro Leu Ser His Lys Val Tyr Met Arg
225 230 235 240

Asn Ser Lys Tyr Pro Gln Asp Leu Val Met Met Glu Gly Lys Met Met
245 250 255

Ser Tyr Cys Thr Thr Gly Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly

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260 265 270

Ala Val Phe Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn Val Ser
275 280 285

Glu Leu Ser Leu Val Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu
290 295 300

Tyr Lys Leu Gly Gly Ser Gly Ser Gly Arg Ser Val Ala His
305 310 315 320

Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro Leu Glu Trp Glu Asp
325 330 335

Thr Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr Lys Gly Gly
340 345 350

Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr
355 360 365

Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro Leu Ser His Lys Val Tyr
370 375 380

Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu Val Met Met Glu Gly Lys
385 390 395 400

Met Met Ser Tyr Cys Thr Thr Gly Gln Met Trp Ala Arg Ser Ser Tyr
405 410 415

Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn
420 425 430

Val Ser Glu Leu Ser Leu Val Asn Phe Glu Glu Ser Gln Thr Phe Phe
435 440 445

Gly Leu Tyr Lys Leu Gly Pro Gly Ser Ser Ser Ser Ser Ala
450 455 460

Trp Ser His Pro Gln Phe Glu Lys
465 470

```

<210> SEQ ID NO 28
<211> LENGTH: 538
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: fusion protein scTRAILwt
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (186) ..(186)
<223> OTHER INFORMATION: Xaa = Ser or Asn
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (188) ..(188)
<223> OTHER INFORMATION: Xaa = Ser or Asn
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (355) ..(355)
<223> OTHER INFORMATION: Xaa = Ser or Asn
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (357) ..(357)
<223> OTHER INFORMATION: Xaa = Ser or Asn

<400> SEQUENCE: 28

```

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Ala Gly Asn Gly Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly
20 25 30

Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu
35 40 45

Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe
50 55 60

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Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys
 65 70 75 80

Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu
 85 90 95

Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr
 100 105 110

Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg
 115 120 125

Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr
 130 135 140

Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser
 145 150 155 160

Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe
 165 170 175

Gly Ala Phe Leu Val Gly Gly Ser Gly Xaa Gly Xaa Gly Ser Arg Val
 180 185 190

Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser
 195 200 205

Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp
 210 215 220

Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg
 225 230 235 240

Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser
 245 250 255

Gln Thr Tyr Phe Arg Phe Gln Glu Ile Lys Glu Asn Thr Lys Asn
 260 265 270

Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp
 275 280 285

Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp
 290 295 300

Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu
 305 310 315 320

Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile
 325 330 335

Asp Met Asp His Glu Ala Ser Phe Gly Ala Phe Leu Val Gly Gly
 340 345 350

Ser Gly Xaa Gly Xaa Gly Ser Arg Val Ala Ala His Ile Thr Gly Thr
 355 360 365

Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys
 370 375 380

Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His
 385 390 395 400

Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His
 405 410 415

Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln
 420 425 430

Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr
 435 440 445

Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser
 450 455 460

Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser
 465 470 475 480

Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe

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485	490	495
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Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser		
500	505	510

Phe Phe Gly Ala Phe Leu Val Gly Gly Pro Gly Ser Ser Ser Ser Ser		
515	520	525

Ser Ala Trp Ser His Pro Gln Phe Glu Lys		
530	535	

<210> SEQ ID NO 29

<211> LENGTH: 546

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: fusion protein sCTAILR2

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<222> LOCATION: (194)..(194)

<223> OTHER INFORMATION: Xaa = Ser or Asn

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<222> LOCATION: (196)..(196)

<223> OTHER INFORMATION: Xaa = Ser or Asn

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<222> LOCATION: (363)..(363)

<223> OTHER INFORMATION: Xaa = Ser or Asn

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<222> LOCATION: (365)..(365)

<223> OTHER INFORMATION: Xaa = Ser or Asn

<400> SEQUENCE: 29

Met Glu Thr Asp Thr Leu Leu Trp Val Leu Leu Leu Trp Val Pro			
1	5	10	15

Ala Gly Asn Gly Ser Pro Gly Ser Ser Ser Ser Ser Arg Val Ala		
20	25	30

Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro		
35	40	45

Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu		
50	55	60

Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn			
65	70	75	80

Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln		
85	90	95

Thr Gln Phe Lys Phe Arg Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp		
100	105	110

Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro		
115	120	125

Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala		
130	135	140

Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys			
145	150	155	160

Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu Arg Leu Leu Gln		
165	170	175

Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Ser		
180	185	190

Gly Xaa Gly Xaa Gly Ser Arg Val Ala Ala His Ile Thr Gly Thr Arg		
195	200	205

Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala		
210	215	220

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Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser
 225 230 235 240

 Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu
 245 250 255

 Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Gln Phe Lys Phe Arg Glu
 260 265 270

 Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile
 275 280 285

 Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala
 290 295 300

 Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile
 305 310 315 320

 Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val
 325 330 335

 Ser Val Thr Asn Glu Arg Leu Leu Gln Met Asp His Glu Ala Ser Phe
 340 345 350

 Phe Gly Ala Phe Leu Val Gly Gly Ser Gly Xaa Gly Xaa Gly Ser Arg
 355 360 365

 Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser
 370 375 380

 Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser
 385 390 395 400

 Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu
 405 410 415

 Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr
 420 425 430

 Ser Gln Thr Gln Phe Lys Phe Arg Glu Glu Ile Lys Glu Asn Thr Lys
 435 440 445

 Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro
 450 455 460

 Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys
 465 470 475 480

 Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu
 485 490 495

 Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu Arg Leu
 500 505 510

 Leu Gln Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
 515 520 525

 Gly Pro Gly Ser Ser Ser Ser Ser Ala Trp Ser His Pro Gln Phe
 530 535 540

Glu Lys
 545

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<210> SEQ_ID NO 30
<211> LENGTH: 1452
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: nucleotide sequence: fusion protein scCD95L

<400> SEQUENCE: 30
aagcttgcgg ccaccatgga gactgacacc ctgctgttg gggtcctact gctttggc 60
cctgcaggaa atggatccga attgcgttagc gtgcacatc tgacaggaaa gtccaacagc 120
agaagtatgc ccctcgaatg ggaggatacc tatgggattg tgctccttc aggcgtgaaa 180
  
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tacaagaagg gtgggctgt catcaatgaa actggattgt acttcgtcta ttcaaagggtt	240
tactttcgta gtcataatcttg taataacttg cctctcagcc ataagggtcta tatgegttaac	300
tccaaataacc cacaagaccc cggttatgtg gagggtaaga ttagttagtta ctgcaccaca	360
ggccaaatgt gggccaggag tagttaccc ggccgggtt ttaacccac tagcgccgat	420
catttgtacg ttaatgtcag cgagctgtcc ttgggtgaact tcgaggaaag ccaaaccatc	480
tttgggttat acaaactcggtt tgccagcggtt agtggctccg gaagaagcgtt cgcacacttg	540
actggcaaataatcccg ttcaatgcctt ctggagtggg aagacactta tggcatcgct	600
ttgctgtctgtgtaaatgtta taagaagggtt ggctgggtt ttaacgaaac cggctgttac	660
ttcgtgtata gcaaaatgttata cttcagagga cagagctgca acaacttgcc tctgtcccat	720
aaagtgtata tgaggaatag taaatatcca caggatctag ttatgtgga agggaaatgt	780
atgtcgattt gtacgaccgg ccagatgtgg gctcgacgca gctatctggg tgccgtattc	840
aacctgtactt ctgcggatca cctctatgtt aacgtgtccg aattgtcgctt ggtgaattt	900
gaggagtcac agacccctt cggactctac aagctgggag gcagtggttag ttggtagccgc	960
cgctctgttgc ttcatactgac gggaaagagc aactcttaga gtatgccctt ggagtgggag	1020
gacacataacg gtatcggtt gttatccggc gttaagtaca agaaaggccg attggtcattc	1080
aacgagactg gactctactt tttctactcg aagggtgtact ttccggccaa atcctgcaac	1140
aaccttccac tctctcacaa ggtctacatcg aggaactcca agtaccacca ggacttgggt	1200
atgtggagg gcaagatgtt gagctactcg actaccggac agatgtgggc acgatccctcg	1260
taccttgggtt ccgtcttcaa cctgacatca gcccaccatc ttttgcgttca cgtcagcgaa	1320
ctgtctctgg tcaacttcga ggaaagtcag acgttcttgc gtttgcgttca gctccgggt	1380
ccctggctcga gtagcagcag ttccagcttgg agtcacccac agttcgagaa gtaataggcg	1440
cgccgcgttca ga	1452

<210> SEQ ID NO 31
 <211> LENGTH: 1650
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: nucleotide sequence: fusion protein scTRAILwt

<400> SEQUENCE: 31	
aagcttgcgc ccaccatgga gactgacacc ctgtgtttt gggcctact gctttgggtc	60
cctgcaggaa atggacagag agtggctgtt cacatcaccc gaaactcgcccc taggtctaac	120
accctgttcca gcccgaattt taagaacgag aaggctctgg gcaggaagat caactcttgg	180
gagttccagca gatccggcata tagtttctgt tctaacttgc acctgagaaa cggcgagctg	240
gtgatccatg agaagggtttt ctactacatc tactctcaga cctacttccg ctttcaggag	300
gagatcaagg agaacaccaa gaacgacaag cagatgggtgc agtacatcta caagtacacc	360
agctatccag acccaatccct gctgtatgtt tccgcttagga actccctgtt gggcaagac	420
gccgagatgtt gcctgtatag catctatcg ggaggcatct tcgagctgaa ggagaacgac	480
aggatcttgc tgagcgttac taatgagcat ctcatacgaca tggaccatgtt agccttttc	540
ttccggcgtt tcttagtggg cgggtccggaa arcgggtartt gtagtgcgtt cgccgcacat	600
attactggca cccggaggag aagtaataact ttgtcaagtc ccaatagcaa gaatggaaag	660
gccctgggtt gaaagatcaa tagctgggag tcaagtcgggtt ctggacacag ctttctcagt	720
aatctccatc tccgaaatgg tgaattggtc atacatgaga aggggttcta ttacatctat	780

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agccaaacctt actttagggtt ccaagaggag attaaggaga acacgaagaa tgataagcag	840
atgggttcaat atatttacaa gtacacttcc tatccagacc cgatcttgct tatgaagtca	900
gcccgtataa gctgttggag taaagatgca gaatacggac tctatagtagt ttaccaaggt	960
gggatatttg aactcaagga gaatgatcgc atattcgat ctgtgacaaa cgaacacttg	1020
attgatatagg accacgaagc tagtttcttc ggagcattcc tgggtggcgg aagcggcart	1080
ggaararcggct ctagagtagc cgccccacata accgggacaaa ggggacgaag caacacgcta	1140
agttctccta actcaaagaa cgagaaagca cttggacgta agatcaactc ctggaaagt	1200
tctcgtatgt ggcattcctt cctgtccaac ctccacttg aaaaatgggg gcttgtgatt	1260
cacgaaaagg gattctacta catctactcc cagacatact tccgattcca agaggaatc	1320
aaggagaata otaagaacga caaacagatg gtccagttaca tatacaagta cacctcatac	1380
cccgatccta tactgttgat gaaatctgca aggaacttctt gctggctaa ggacgctgag	1440
tatgggttgt actcgatcta ccaggggcgg aaaaaatcgatgt tgaaagagaa cgaccgcata	1500
ttcgtgtcag taaccaacga gcacctgata gatatggacc atgaggcatc cttcttttgt	1560
gccttcotgg tgggggggtcc tggctcgagt agcagcagtt cagcttggag tcacccacag	1620
ttcgagaagt aataggcgcg ccgcgcgtac	1650

<210> SEQ ID NO 32
 <211> LENGTH: 1674
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: nucleotide sequence: fusion protein scTRAILR2

<400> SEQUENCE: 32	
aagcttgcgc ccaccatgga gactgacacc ctgctgttgt gggtcctact gctttgggtc	60
cctgcaggaa atggatcccc tggagttct tcaagctcta gcagagtggc tgctcacatc	120
accggaaactc ggggttaggtc taacaccctg tccagcccgaa attccaagaa cgagaaggct	180
ctgggcaggaa agatcaactc ttgggagttcc agcagatccg gtcatagttt cctgtctaac	240
ttgcacctga gaaacggcga gctggtgatc catgagaagg gtttctacta catctactct	300
cagacccagt tcaagttcg ggaggagatc aaggagaaca ccaagaacga caagcagatg	360
gtgcagtaca tctacaagta caccagctat ccagacccaa tctgtgtat gaagtccgct	420
aggaactcct gttggagcaa agacgcccggat tatggctgtt atagcatcta tcagggggc	480
atcttcgagc tgaaggagaa cgacaggatc ttctgtgatc tcaactatga gaggctgctc	540
cagatggacc atgaaggctc ttttttcggc gctttcttag tgggggggttc cggaarcgg	600
artggtagtc gcgtcgccgc acatattact ggcacccggag ggagaagtaa tactttgtca	660
agtccccata gcaagaatga gaaggccctg ggtcgaaaga tcaatagctg ggagtcaagt	720
cggtctggac acagcttct cagtaatctc catctccgaa atggtaattt ggtcatacat	780
gagaaggggt tctattacat ctatagccaa actcagtttta agttccgaga ggagattaag	840
gagaacacga agaatgataa gcagatgggtt caatataattt acaagtacac ttccatatcca	900
gaccggatct tgcttatgaa gtcagcccgat aatagctgtt ggagtaaga tgcaataac	960
ggactctata gtatattacca aggtgggata tttgaactca aggagaatga tcgcataattc	1020
gtatctgtga caaacgaacg cttgtttcag atggaccacg aagctagttt cttcgagca	1080
ttcctgggtgg gcggaaagcgg cartggaaarc ggctctagag tagccgcccc cataaccgg	1140

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acaaggggac gaagcaacac gctaaggctt cctaactcaa agaacgagaa agcacttgg	1200
cgttaagatca actccctggga aagttctcggt agtgggcatt ctttcctgtc caacccac	1260
ttgagaaaatg gggagttgt gattcacgaa aaggattct actacatcta ctcccagaca	1320
cagttcaaat tccgagagga aatcaaggag aatactaaga acgacaaaca gatggtcag	1380
tacatataaca agtacacccat atacccat cctatactgt tgatgaaatc tgcaaggAAC	1440
tcttgcgtgt ctaaggacgc tgagtatggg ttgtactcgta tctaccaggcg gggatTTT	1500
gagttgaaag agaacgaccg catattcgta tcagtaacca acgagcgctt gttcagatg	1560
gaccatgagg catcccttgggcttc ctggggcg gtcctggctc gagtagcagc	1620
agttcagtt ggagtcaccc acagttcgag aagtaatagg cgccggcgtagc	1674

<210> SEQ_ID NO 33
<211> LENGTH: 222
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: pertuzumab Fab-Heavy Chain modul (VHCH1)

<400> SEQUENCE: 33

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly			
1	5	10	15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Asp Tyr			
20	25	30	

Thr Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val			
35	40	45	

Ala Asp Val Asn Pro Asn Ser Gly Gly Ser Ile Tyr Asn Gln Arg Phe			
50	55	60	

Lys Gly Arg Phe Thr Leu Ser Val Asp Arg Ser Lys Asn Thr Leu Tyr			
65	70	75	80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	

Ala Arg Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr Trp Gly Gln Gly			
100	105	110	

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe			
115	120	125	

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu			
130	135	140	

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp			
145	150	155	160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu			
165	170	175	

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser			
180	185	190	

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro			
195	200	205	

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys			
210	215	220	

<210> SEQ_ID NO 34
<211> LENGTH: 214
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: pertuzumab Fab-Light Chain modul (VLCL)

<400> SEQUENCE: 34

-continued

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Ile Gly
 20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Ile Tyr Pro Tyr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> SEQ ID NO 35
 <211> LENGTH: 16
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: human IgG1 hinge region

<400> SEQUENCE: 35

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
 1 5 10 15

<210> SEQ ID NO 36
 <211> LENGTH: 263
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: pertuzumab scFv-module

<400> SEQUENCE: 36

Met Glu Thr Asp Thr Leu Leu Trp Val Leu Leu Trp Val Pro
 1 5 10 15

Ala Gly Asn Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
 20 25 30

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
 35 40 45

Phe Thr Asp Tyr Thr Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly
 50 55 60

Leu Glu Trp Val Ala Asp Val Asn Pro Asn Ser Gly Gly Ser Ile Tyr

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65	70	75	80
Asn Gln Arg Phe Lys Gly Arg Phe Thr Leu Ser Val Asp Arg Ser Lys			
85	90	95	
Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala			
100	105	110	
Val Tyr Tyr Cys Ala Arg Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr			
115	120	125	
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser			
130	135	140	
Gly Gly Gly Ser Gly Gly Ser Asp Ile Gln Met Thr Gln			
145	150	155	160
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr			
165	170	175	
Cys Lys Ala Ser Gln Asp Val Ser Ile Gly Val Ala Trp Tyr Gln Gln			
180	185	190	
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Tyr Arg			
195	200	205	
Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp			
210	215	220	
Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr			
225	230	235	240
Tyr Cys Gln Gln Tyr Tyr Ile Tyr Pro Tyr Thr Phe Gly Gln Gly Thr			
245	250	255	
Lys Val Glu Ile Lys Arg Thr			
260			

<210> SEQ_ID NO 37
<211> LENGTH: 230
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: human IgG1 Fc part (hinge+CH2+CH3)

<400> SEQUENCE: 37

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu			
1	5	10	15
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp			
20	25	30	
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp			
35	40	45	
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly			
50	55	60	
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn			
65	70	75	80
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp			
85	90	95	
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro			
100	105	110	
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu			
115	120	125	
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn			
130	135	140	
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile			
145	150	155	160
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr			

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165 170 175

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
180 185 190

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
195 200 205

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
210 215 220

Ser Leu Ser Pro Gly Lys
225 230

<210> SEQ ID NO 38
<211> LENGTH: 246
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: N-terminal Fc-module with signal peptide

<400> SEQUENCE: 38

Met	Glu	Thr	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro
1				5					10					15	

Ala Gly Asn Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
20 25 30

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 35 40 45

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
50 55 60

Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp
65				70					75						80

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
85 90 95

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
100 105 110

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
 115 120 125

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
130 135 140

Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys
145					150					155					160

Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp
				165					170					175	

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
180 185 190

Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser
		195					200						205		

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 210 215 220

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
225 230 235 240

Leu Ser Leu Ser Pro Gly
245

<210> SEQ ID NO 3

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: pertuzumab Fab heavy chain module with signal

-continued

peptide

<400> SEQUENCE: 39

Met	Glu	Thr	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro
1					5				10				15		

Ala	Gly	Asn	Gly	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Leu	Val	
					20			25				30			

Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr
					35		40		45						

Phe	Thr	Asp	Tyr	Thr	Met	Asp	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly
					50		55		60						

Leu	Glu	Trp	Val	Ala	Asp	Val	Asn	Pro	Asn	Ser	Gly	Gly	Ser	Ile	Tyr
65						70		75					80		

Asn	Gln	Arg	Phe	Lys	Gly	Arg	Phe	Thr	Leu	Ser	Val	Asp	Arg	Ser	Lys
					85		90		95						

Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala
					100			105		110					

Val	Tyr	Tyr	Cys	Ala	Arg	Asn	Leu	Gly	Pro	Ser	Phe	Tyr	Phe	Asp	Tyr
					115		120		125						

Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly
					130		135		140						

Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly
145					150			155		160					

Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val
					165		170		175						

Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe
					180		185		190						

Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val
					195		200			205					

Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val
					210		215		220						

Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys
					225		230			235		240			

Ser	Cys	Asp	Lys	Thr	His	Gly	Ser	Pro	Gly	Ser	Ser	Ser	Ser	Ser	
					245		250			255					

Ala	Trp	Ser	His	Pro	Gln	Phe	Glu	Lys
					260		265	

<210> SEQ_ID NO 40

<211> LENGTH: 253

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: pertuzumab Fab light chain module with signal peptide

<400> SEQUENCE: 40

Met	Glu	Thr	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro
1					5			10				15			

Gly	Ser	Thr	Gly	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser
					20		25			30					

Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Asp
					35		40		45						

Val	Ser	Ile	Gly	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro
					50		55			60					

Lys Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Ser

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65	70	75	80
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser			
85	90	95	
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr			
100	105	110	
Ile Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg			
115	120	125	
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln			
130	135	140	
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr			
145	150	155	160
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser			
165	170	175	
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr			
180	185	190	
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys			
195	200	205	
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro			
210	215	220	
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Ser Pro Gly Ser Ser			
225	230	235	240
Ser Ser Ser Ser Ala Trp Ser His Pro Gln Phe Glu Lys			
245	250		

<210> SEQ ID NO 41
 <211> LENGTH: 823
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: pertuzumab Fab heavy chain gene module

<400> SEQUENCE: 41

aagcttgcgg ccaccatgga gactgacacc ctgctgtgt gggtcctact gctttggc	60
cctgcaggta acggtaaagt gcacgtcgta gaaagcgggt gccggactgg tcageccgg	120
ggttctctgc ggctgtcttg tgctgcctcg ggttcacgt tcactgacta cacaatggac	180
tgggtgcgtc aggctcctgg aaaggaggatt gagtgggtag ccgacgttaa tccaaactcc	240
ggcgggagca tctacaacca gaggttcaag gggaggtca ctctgagcgt ggatcgctcc	300
aagaacacgc tgtacctcca gatgaactct ctcaggccgc aggacacggc tgtttactat	360
tgcgcgagga acctgggtcc ttccctctac ttcgactact ggggacaggg aaccctgg	420
accgtcagct ccgcttctac caagggtctc agtgtgtcc ctcttgctcc cagctctaaa	480
agcacctccg gtggaaactgc tgctctgggc tgctctggta aggactactt ccccaacccc	540
gtgaccgtat cttggaaactc cggcgcactt acttctggcg tccacacttt cccagccgtc	600
ttacagtccct ctggcctgtta ttctttgagc agcgtcgtga ccgtgcctag cagtagtctg	660
ggcacccaga octacatctg caacgtcaac cacaagccta gcaacaccaa gggtgacaag	720
aagggtcgagc otaagtcgtg cgacaagacg cacggatccc ctggctcgag ttcaagctct	780
tctgcctggc cacatccaca attcgagaag taataggcgc gcc	823

<210> SEQ ID NO 42
 <211> LENGTH: 787
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:

-continued

<223> OTHER INFORMATION: pertuzumab Fab light chain gene module

<400> SEQUENCE: 42

aagcttgcggcc	ccaccatggaa	gaccgataca	ctgctttgt	gggtactctt	gctgtgggtt	60
ccgggatcta	ccgggtacat	ccagatgaca	caatctccta	gcagtctgag	cgcaagtgtt	120
ggagatcgtg	tcaccatcac	atgcaaggcc	agccaggatg	tgagcattgg	agtcgcctgg	180
tatcagcaga	aacccggcaa	ggcacccaa	ctgctgtatc	actcggccag	ttacagatac	240
actggcgtac	cttcgagggtt	tagtggtagc	ggttctggaa	ccgattcac	cctcaccatt	300
agctccctcc	aacccgagga	cttcgcccacc	tactactgccc	agcaataacta	catctacccct	360
tacacgttgc	gccaaaggcac	taaggtcgag	attaaacgta	cggtcgac	tcctccgt	420
ttcatcttcc	cacctagcga	cgagcagcta	aagtctggaa	ctgcgtccgt	cgtgtgcctg	480
ctcaacaact	tctaccctcg	ggaagcgaag	gtccagtgaa	aagtggacaa	cgctctccag	540
tccggcaata	gccaggaatc	cgtgaccgag	caggacagca	aggattctac	ctactcactg	600
tccagcaccc	ttacgctgtc	caaggccgac	tacgagaagc	ataagggtgt	cgcttgcgt	660
gtgactcacc	aaggctgtc	aaggccctgt	accaagagct	tcaacagagg	cgagtgcgg	720
tcccctggct	cgagttcaag	ctcttctgcc	tggtcacatc	cacaattcga	gaagtaatag	780
gcgcgc						787

<210> SEQ ID NO 43

<211> LENGTH: 771

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: scTRAILwt-Fc fusion protein with signal peptide

<400> SEQUENCE: 43

Met	Glu	Thr	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro
1					5			10					15		

Ala	Gly	Asn	Gly	Gln	Arg	Val	Ala	Ala	His	Ile	Thr	Gly	Thr	Arg	Gly
						20			25			30			

Arg	Ser	Asn	Thr	Leu	Ser	Ser	Pro	Asn	Ser	Lys	Asn	Glu	Lys	Ala	Leu
						35		40		45					

Gly	Arg	Lys	Ile	Asn	Ser	Trp	Glu	Ser	Ser	Arg	Ser	Gly	His	Ser	Phe
						50		55		60					

Leu	Ser	Asn	Leu	His	Leu	Arg	Asn	Gly	Glu	Leu	Val	Ile	His	Glu	Lys
						65		70		75		80			

Gly	Phe	Tyr	Tyr	Ile	Tyr	Ser	Gln	Thr	Tyr	Phe	Arg	Phe	Gln	Glu	Glu
						85		90		95					

Ile	Lys	Glu	Asn	Thr	Lys	Asn	Asp	Lys	Gln	Met	Val	Gln	Tyr	Ile	Tyr
						100		105		110					

Lys	Tyr	Thr	Ser	Tyr	Pro	Asp	Pro	Ile	Leu	Leu	Met	Lys	Ser	Ala	Arg
						115		120		125					

Asn	Ser	Cys	Trp	Ser	Lys	Asp	Ala	Glu	Tyr	Gly	Leu	Tyr	Ser	Ile	Tyr
						130		135		140					

Gln	Gly	Gly	Ile	Phe	Glu	Leu	Lys	Glu	Asn	Asp	Arg	Ile	Phe	Val	Ser
						145		150		155		160			

Val	Thr	Asn	Glu	His	Leu	Ile	Asp	Met	Asp	His	Glu	Ala	Ser	Phe	Phe
						165		170		175					

Gly	Ala	Phe	Leu	Val	Gly	Gly	Ser	Gly	Asn	Gly	Ser	Arg	Val		
						180		185		190					

Ala	Ala	His	Ile	Thr	Gly	Thr	Arg	Gly	Arg	Ser	Asn	Thr	Leu	Ser	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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195	200	205
Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp		
210	215	220
Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg		
225	230	235
240		
Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser		
245	250	255
Gln Thr Tyr Phe Arg Phe Gln Glu Ile Lys Glu Asn Thr Lys Asn		
260	265	270
Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp		
275	280	285
Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp		
290	295	300
Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu		
305	310	315
320		
Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile		
325	330	335
Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly		
340	345	350
Ser Gly Ser Gly Asn Gly Ser Arg Val Ala Ala His Ile Thr Gly Thr		
355	360	365
Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys		
370	375	380
Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His		
385	390	395
400		
Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His		
405	410	415
Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln		
420	425	430
Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr		
435	440	445
Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser		
450	455	460
Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser		
465	470	475
480		
Ile Tyr Gln Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe		
485	490	495
Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser		
500	505	510
Phe Phe Gly Ala Phe Leu Val Gly Gly Pro Gly Ser Ser Ser Ser		
515	520	525
Ser Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro		
530	535	540
Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr		
545	550	555
560		
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val		
565	570	575
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val		
580	585	590
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser		
595	600	605
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu		
610	615	620

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Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser
625															640
Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro
															655
Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln
															670
Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala
															685
Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	lys	Thr	Thr
															700
Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu
															720
Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser
															735
Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser
															750
Leu	Ser	Pro	Gly	Ser	Ser	Ser	Ser	Ser	Ser	Ala	Trp	Ser	His	Pro	Gln
															765
Phe	Glu	Lys													
															770

<210> SEQ ID NO 44
<211> LENGTH: 2341
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: scTRAILwt-FC01 gene module

<400> SEQUENCE: 44

aagcttgcggccaccatggaa	gactgacacc	ctgtgttgtt	gggtcctact	gctttgggtc	60
cctgcaggaa	atggacagag	agtggctgt	cacatcaccc	gaactcgaaaa	120
accctgtcca	gccccgaaattc	taagaacgag	aaggctctgg	gcaggaagat	180
gagtcagca	gatccggta	tagttccctg	tctaacttgc	accttgaaaa	240
gtgatccatg	agaaggcgtt	ctactacatc	tactctcaga	cctacttccg	300
gagatcaagg	agaacaccaa	gaacgacaag	cagatgggtc	agtatcatct	360
agctatccag	acccaatcc	gctgatgaa	tccgcttagg	actcctgttg	420
gccgagatgt	gcctgtatag	catctatcg	ggaggcatct	tgcagatgaa	480
aggatcttcg	tgagcgtcac	taatgagcat	ctcatcgaca	tggaccatga	540
ttcggcgctt	tcttagtggg	cggttccgga	agcggtatg	gtatcgctgt	600
atactggca	cccgaggggag	aagtaatact	ttgtcaagtc	ccaatagcaa	660
gccctgggtc	gaaagatcaa	tagctggag	tcaagtcgg	ctggacacag	720
aatctccatc	tccgaaatgg	tgaattggtc	atacatgaga	aggggttcta	780
agccaaacctt	actttagggtt	ccaagaggag	attaaggaga	acacgaagaa	840
atgggtcaat	atatttacaa	gtacacttcc	tatccagacc	cgatcttgc	900
gcccgtaata	gctgtggag	taaagatgca	gaatacggac	tctatagtat	960
ggatattttg	aactcaagga	gaatgatcgc	atattcgat	ctgtgacaaa	1020
attgatatgg	accacgaagc	tagttctc	ggagcattcc	tggtggggcgg	1080
ggaaacggct	ctagagtagc	cggccacata	accgggacaa	ggggacgaag	1140

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agttctccta actcaaagaa cgagaaagca ctggacgta agatcaactc ctggaaagt	1200
tctcgtagtg ggcattcctt cctgtccaac ctccacttgaa gaatgggga gcttgtgatt	1260
cacgaaaagg gattctacta catctactcc cagacatact tccgattcca agaggaatc	1320
aaggagaata ctaagaacga caaacagatg gtccagatcata tatacaagta cacctcatac	1380
cccgatccta tactgttcat gaaatctgca aggaactctt gctggctaa ggacgctgag	1440
tatgggttgt actcgatcta ccagggcggaa atttcgagt tgaaagagaa cgaccgcata	1500
ttcgtgtcag taaccaacga gcacctgata gatatggacc atgaggcata ctttttgt	1560
gccttcctgg tggcgggtcc tggctcgagt agctcctcat ccggctccga taagaccac	1620
acctgcctc cctgtcctgc ccctcctgtc gctggaccta gcgtgttccct gttccctcca	1680
aaggcctaagg acaccctgtat gatctccagg acccctgagg tgacctgtgt ggtggtgac	1740
gtgtctcactg aagatcccga ggtgaagttc aactggtagc tggacggcgt ggagggtccac	1800
aacgccaaga ccaagccctag ggaggagcag tacaactcca cctaccgggt ggtgtctgt	1860
ctgaccgtgc tgcaccaggaa ttggctgaac gggaaaggagt ataagttaa ggtctccaaac	1920
aaggggctgc cttcatctat cgagaaaacc atctccaagg ccaagggcca gcctcggag	1980
cctcagggtgt acaccctgcc tccttagcagg gaggagatga ccaagaacca ggtgtccctg	2040
acctgtctgg tgaagggctt ctacccttcc gatatcgccc tggagtgaaa gtctaatggc	2100
cagccccaga acaactacaa gaccacccct cctgtgttgg actctgacgg ctccttcc	2160
ctgtactcca agctgaccgtt ggacaagtcc agatggcagc agggcaacgt gttctctgc	2220
tccgtgtatgc acgaggccct gcacaatcac tacacccaga agtccctgtc tctgatccg	2280
ggctcatctt caagctttc tgccctggct catccgaat tcgagaaata ataggcgcgc	2340
c	2341

<210> SEQ_ID NO 45

<211> LENGTH: 773

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: HC-scTRAILwt-SNSN

<400> SEQUENCE: 45

Met	Glu	Thr	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro
1					5				10				15		

Ala	Gly	Asn	Gly	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val
					20			25				30			

Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr
					35		40		45						

Phe	Thr	Asp	Tyr	Thr	Met	Asp	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly
					50		55		60						

Leu	Glu	Trp	Val	Ala	Asp	Val	Asn	Pro	Asn	Ser	Gly	Gly	Ser	Ile	Tyr
					65		70		75				80		

Asn	Gln	Arg	Phe	Lys	Gly	Arg	Phe	Thr	Leu	Ser	Val	Asp	Arg	Ser	Lys
					85		90		95						

Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala
					100			105				110			

Val	Tyr	Tyr	Cys	Ala	Arg	Asn	Leu	Gly	Pro	Ser	Phe	Tyr	Phe	Asp	Tyr
					115		120		125						

Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly
					130		135		140						

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Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 145 150 155 160
 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 165 170 175
 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 180 185 190
 Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 195 200 205
 Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
 210 215 220
 Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
 225 230 235 240
 Ser Cys Asp Lys Thr His Gly Ser Pro Gly Ser Ser Ser Ser Ser
 245 250 255
 Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
 260 265 270
 Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
 275 280 285
 Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
 290 295 300
 Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
 305 310 315 320
 Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
 325 330 335
 Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
 340 345 350
 Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
 355 360 365
 Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
 370 375 380
 Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
 385 390 395 400
 Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
 405 410 415
 Gly Gly Ser Gly Asn Gly Ser Arg Val Ala Ala His Ile Thr
 420 425 430
 Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn
 435 440 445
 Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser
 450 455 460
 Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val
 465 470 475 480
 Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg
 485 490 495
 Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val
 500 505 510
 Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met
 515 520 525
 Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu
 530 535 540
 Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg
 545 550 555 560
 Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu

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565	570	575
Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly Ser Gly Ser Gly Asn		
580	585	590
Gly Ser Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn		
595	600	605
Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys		
610	615	620
Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn		
625	630	635
Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr		
645	650	655
Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu		
660	665	670
Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr		
675	680	685
Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys		
690	695	700
Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly		
705	710	715
Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn		
725	730	735
Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe		
740	745	750
Leu Val Gly Gly Pro Gly Ser Ser Ser Ser Ser Ala Trp Ser His		
755	760	765
Pro Gln Phe Glu Lys		
770		

<210> SEQ ID NO 46
<211> LENGTH: 2347
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: HC-scTRAILwt-SNSN gene module

<400> SEQUENCE: 46

aagcttgcgg ccaccatgga gactgacacc ctgctgttg gggctctact gctttggc	60
cctgcaggta acggtaagt gcagctcg tc gaaagcggtg gccggacttgt tcagcccggt	120
ggttctctgc ggctgtcttg tgctgcctcg ggttcacgt tcactgacta cacaatggac	180
tgggtgcgtc aggctcctgg aaaggattg gagtggttag ccgacgttaa tccaaactcc	240
ggcggggagca tctacaacca gaggttcaag gggaggtca ctctgagcgt ggatcgctcc	300
aagaacacgc tgcgttcca gatgactct ctcaggccg aggacacgc tgttactat	360
tgcgcgagga acctgggtcc ttccctctac ttgcactact ggggacaggg aaccctggtg	420
accgtcagct ccgcttctac caagggtct agtgtgttcc ctcttgcgtc cagctctaaa	480
agcacctccg gtggaaactgc tgctctggc tgtctggta aggactactt ccccgaaccc	540
gtgaccgtat ttggaaactc cggcgactt acttctggcg tccacactt cccagccgtc	600
ttacagtccct ctggcctgtt ttctttgacg agcgtcgta ccgtgcctag cagtagtctg	660
ggcaccacaga cctacatctg caacgtcaac cacaagccta gcaacaccaa gttgacaag	720
aagggtcgacg ctaagtcgtg cgacaagacg cacggatccc ctggaaagttc ttcaagctct	780
agcagagtggtt ctgctcacat caccggaaact cggggtaggtt ctaacaccct gtccagcccc	840

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aattctaaga acgagaaggc tctgggcagg aagatcaact cttgggagtc cagcagatcc	900
ggtcatagtt tcctgtctaa cttgcacctg agaaacggcg agctgggtat ccatgagaag	960
ggcttctact acatctactc tcagacctac ttccgcttc aggaggagat caaggagaac	1020
accaagaacg acaaggcagat ggtgcagttac atctacaagt acaccagcta tccagaccca	1080
atcctgctga tgaagtccgc taggaactcc tggtggagca aagacgcccga gtatggctg	1140
tatagcatct atcaggaggc catcttcgag ctgaaggaga acgacaggat ctgcgtgagc	1200
gtcactaatg agcatctcat cgacatggac catgaagecct ctttcttcgg cgctttctta	1260
gtggggcggtt ccggaaagccgg taatggtagt cgcgctcgccg cacatattac tggcaccgg	1320
gggagaagta atactttgtc aagtcccaat agcaagaatg agaaggccct gggtcgaaag	1380
atcaatagct gggagtcaag tcggctctgga cacagcttc tcaatgccttccat	1440
aatggtgaat tggcatacata tgagaagggg ttcttattaca tctatagccaaacttactt	1500
aggttccaag aggagattaa ggagaacacg aagaatgata agcagatggt tcaatatatt	1560
tacaagtaca cttccatcc agacccgatc ttgcattatga agtcagcccg taatagctgt	1620
tggagtaaag atgcagaata cggactctat agtatttacc aaggtggat atttgaactc	1680
aaggagaatg atcgcattt cgtatctgtg acaaacgaac acttgattga tatggaccac	1740
gaagcttagtt tcttcggagc atttcctgggt ggcggaaagcg gcagtgaaaa cggctctaga	1800
gtagccgcccc acataaccgg gacaagggga cgaagcaaca cgctaagtcc tccttaactca	1860
aagaacgaga aagcacccgg acgtaaatgc aactccctggg aaagttctcg tagtggcat	1920
tccttcctgt ccaaccccca cttgagaaat gggagcttg tgattcacga aaaggggattc	1980
tactacatct actcccaagac atactccga ttccaagagg aaatcaagga gaatactaag	2040
aacgacaaac agatggtcca gtacatatac aagtacacccct catacccccga tcctataactg	2100
ttgatgaaat ctgcaaggaa ctcttgctgg tctaaggacg ctgagttatgg gttgtactcg	2160
atctaccagg gcgaaatttt cgagttgaaa gagaacgacc gcataattcgt gtcagtaacc	2220
aacgagcacc tgatagatggat ggaccatgag gcataccctt ttgggtgcctt cctggggc	2280
ggtcctggctt cgagtagcag cagttcagct tggagtaccaccacatcgaa gaagtaatag	2340
gcccccc	2347

<210> SEQ ID NO 47
 <211> LENGTH: 773
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: HC-scTRAILR2-SNSN with signal peptide

<400> SEQUENCE: 47

Met	Glu	Thr	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro
1					5				10				15		

Ala	Gly	Asn	Gly	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Ley	Val
					20			25				30		

Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr
					35			40				45			

Phe	Thr	Asp	Tyr	Thr	Met	Asp	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly
					50			55				60			

Leu	Glu	Trp	Val	Ala	Asp	Val	Asn	Pro	Asn	Ser	Gly	Gly	Ser	Ile	Tyr
					65			70			75			80	

Asn	Gln	Arg	Phe	Lys	Gly	Arg	Phe	Thr	Leu	Ser	Val	Asp	Arg	Ser	Lys
					85			90			95				

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Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
 100 105 110
 Val Tyr Tyr Cys Ala Arg Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr
 115 120 125
 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
 130 135 140
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 145 150 155 160
 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 165 170 175
 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 180 185 190
 Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 195 200 205
 Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
 210 215 220
 Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
 225 230 235 240
 Ser Cys Asp Lys Thr His Gly Ser Pro Gly Ser Ser Ser Ser Ser
 245 250 255
 Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
 260 265 270
 Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
 275 280 285
 Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
 290 295 300
 Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
 305 310 315 320
 Tyr Ser Gln Thr Gln Phe Lys Phe Arg Glu Glu Ile Lys Glu Asn Thr
 325 330 335
 Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
 340 345 350
 Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
 355 360 365
 Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
 370 375 380
 Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu Arg
 385 390 395 400
 Leu Leu Gln Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
 405 410 415
 Gly Gly Ser Gly Ser Gly Asn Gly Ser Arg Val Ala Ala His Ile Thr
 420 425 430
 Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn
 435 440 445
 Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser
 450 455 460
 Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val
 465 470 475 480
 Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Gln Phe Lys
 485 490 495
 Phe Arg Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val
 500 505 510

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Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met
515 520 525

Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu
530 535 540

Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg
545 550 555 560

Ile Phe Val Ser Val Thr Asn Glu Arg Leu Leu Gln Met Asp His Glu
565 570 575

Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly Ser Gly Ser Gly Asn
580 585 590

Gly Ser Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn
595 600 605

Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys
610 615 620

Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn
625 630 635 640

Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr
645 650 655

Tyr Ile Tyr Ser Gln Thr Gln Phe Lys Phe Arg Glu Glu Ile Lys Glu
660 665 670

Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr
675 680 685

Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys
690 695 700

Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly
705 710 715 720

Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn
725 730 735

Glu Arg Leu Leu Gln Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe
740 745 750

Leu Val Gly Gly Pro Gly Ser Ser Ser Ser Ser Ala Trp Ser His
755 760 765

Pro Gln Phe Glu Lys
770

<210> SEQ ID NO 48
<211> LENGTH: 2347
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: HC-scTRAILR2-SNSN gene module

<400> SEQUENCE: 48

```
aagcttgcggccacccatggaaactgacaccctgtgtttgtgggtcctactgcgttgggtc 60
cctgcaggtaacggtaaagtgcagtcgtcgaaagcggtgcggactggttcagcccggt 120
ggttctctgcggctgttttgctgcctcggtttcacgttcactgactacaatggac 180
tgggtgcgtcaggctctggaaaggatttgagtggttagccgacgttaatccaaactcc 240
ggcgccggcactacaaccaaggttcaagggagggtcaactcgacgtggatcgctcc 300
aagaacacgcgttacccatccatgttactcttcaggcccaggacacggcgtttactat 360
tgcgcgaggaacctgggtccttccttctacttcgactactggggacagggaaacctgttg 420
accgtcagctccgttctaccaagggttccatgttgcgttcccttgcgttccatgttctaaa 480
aaccacccatccgttggaaactgcgttgcgttgggttcaaggactacttccccgaaccc 540
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gtgaccgtat cttggaactc cggegcactt acttctggcg tccacactt cccagccgtc	600
ttacagtctt ctggcctgtt ttcttgac agcgtcgatg cctgtccatg cagtagtctg	660
ggcacccaga octacatctg caacgtcaac cacaagecta gcaacaccaa gggtgacaag	720
aaggtegacg ctaagtcgtg cgacaagacg cacggatccc ctggaagttc ttcaagctct	780
agcagagtgg ctgctcacat caccggaaact cggggtaggt ctaacaccct gtccagcccg	840
aattccaaga acgagaaggc tctggcagg aagatcaact ctggggagtc cagcagatcc	900
ggtcatagtt tcctgtctaa cttgcacctg agaaacggcg agctggtgat ccatgagaag	960
ggcttctact acatctactc tcagacccag ttcaagttc gggaggagat caaggagaac	1020
accaagaacg acaagcagat ggtgcagttc atctacaagt acaccagcta tccagaccca	1080
atcctgtgtg tgaagtccgc taggaactcc tggtggagca aagacgcccgtatggcctg	1140
tatagcatct atcagggagg catcttcgag ctgaaggaga acgacaggat ctctgtgagc	1200
gtcactaatg agaggctgct ccagatggac catgaagccct ctttcttcgg cgctttctta	1260
gtggggcggtt cccggaaacggg taatggtagt cgcgtcgccg cacatattac tggcaccgcg	1320
gggagaagta atactttgtc aagtcccaat agcaagaatg agaaggccct gggtcgaaag	1380
atcaatagct gggagtcaag tcggctctgga cacagtttc tcagtaatct ccatctccga	1440
aatggtaat tggtcataca tgagaagggg ttcttattaca tctatagcca aactcagttt	1500
aagttccgag aggagattaa ggagaacacg aagaatgata agcagatggt tcaatatatt	1560
tacaagtaca cttcctatcc agacccgatc ttgcttatga agtcagcccg taatagctgt	1620
tggagtaaag atgcagaata cggactctat agtatttacc aagggtggat atttgaactc	1680
aaggagaatg atcgcatatt cgtatctgtg acaaacgaac gcttgcattca gatggaccac	1740
gaagctagtt tcttcggagc attcctgggt ggcggaaacgc gcagtgaaa cggctctaga	1800
gtagccgcc acataaccgg gacaagggga cgaagcaaca cgcttaagttc tcctaactca	1860
aagaacgaga aagcacttgg acgtaagatc aactcctggg aaagttctcg tagtggcat	1920
tccttcctgt ccaaccccca cttgagaaat gggagcttg tgattcacga aaagggattc	1980
tactacatct actcccaagac acatgtcaaa ttccgagagg aaatcaagga gaatactaag	2040
aacgacaaac agatggtcca gtacatatac aagtacacct catacccgat tcctataactg	2100
ttgatgaaat ctgcaaggaa ctcttgctgg tctaaggacg ctgagttatgg gttgtactcg	2160
atctaccagg gcggaaatttt cgagttgaaa gagaacgacc gcatattcgt gtcagtaacc	2220
aacgagccgc ttggcagat ggaccatgag gcatccttct ttgggtgcctt cctggggc	2280
ggtcctggct cgagtagcag cagttcagct tggagtcacc cacagttcga gaagtaatag	2340
gcggcc	2347

<210> SEQ ID NO 49
 <211> LENGTH: 773
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: HC-scTRAILR2-SSSS with signal peptide

<400> SEQUENCE: 49

Met	Glu	Thr	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro
1					5				10				15		

Ala	Gly	Asn	Gly	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Ley	Val	
20					25								30		

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr

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35	40	45
Phe Thr Asp Tyr Thr Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly		
50	55	60
Leu Glu Trp Val Ala Asp Val Asn Pro Asn Ser Gly Gly Ser Ile Tyr		
65	70	75
Asn Gln Arg Phe Lys Gly Arg Phe Thr Leu Ser Val Asp Arg Ser Lys		
85	90	95
Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala		
100	105	110
Val Tyr Tyr Cys Ala Arg Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr		
115	120	125
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly		
130	135	140
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly		
145	150	155
160		
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val		
165	170	175
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe		
180	185	190
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val		
195	200	205
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val		
210	215	220
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys		
225	230	235
240		
Ser Cys Asp Lys Thr His Gly Ser Pro Gly Ser Ser Ser Ser Ser Ser		
245	250	255
Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu		
260	265	270
Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn		
275	280	285
Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His		
290	295	300
Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile		
305	310	315
320		
Tyr Ser Gln Thr Gln Phe Lys Phe Arg Glu Glu Ile Lys Glu Asn Thr		
325	330	335
Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr		
340	345	350
Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser		
355	360	365
Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe		
370	375	380
Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu Arg		
385	390	395
400		
Leu Leu Gln Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val		
405	410	415
Gly Gly Ser Gly Ser Gly Ser Arg Val Ala Ala His Ile Thr		
420	425	430
Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn		
435	440	445
Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser		
450	455	460

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Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val
465 470 475 480

Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Gln Phe Lys
485 490 495

Phe Arg Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val
500 505 510

Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met
515 520 525

Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu
530 535 540

Tyr Ser Ile Tyr Gln Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg
545 550 555 560

Ile Phe Val Ser Val Thr Asn Glu Arg Leu Leu Gln Met Asp His Glu
565 570 575

Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly Ser Gly Ser Gly Ser
580 585 590

Gly Ser Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn
595 600 605

Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys
610 615 620

Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn
625 630 635 640

Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr
645 650 655

Tyr Ile Tyr Ser Gln Thr Gln Phe Lys Phe Arg Glu Glu Ile Lys Glu
660 665 670

Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr
675 680 685

Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys
690 695 700

Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly
705 710 715 720

Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn
725 730 735

Glu Arg Leu Leu Gln Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe
740 745 750

Leu Val Gly Gly Pro Gly Ser Ser Ser Ser Ser Ala Trp Ser His
755 760 765

Pro Gln Phe Glu Lys
770

<210> SEQ ID NO 50

<211> LENGTH: 2347

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: HC-scTRAILR2-SSSS gene module

<400> SEQUENCE: 50

aagcttgccg ccaccatgg aactgacacc ctgctgtgt gggtcctact gctttgggtc 60

cctgcaggta acgggtaaat gcagctcgta gaaagcggtt gcgacttgt tcagccccgt 120

ggttctctgc ggctgtcttg tgctgcctcg ggtttacagt tcactgacta cacaatggac 180

tgggtgcgtc aggctcctgg aaagggattt gagtggttag ccgacgttaa tccaaactcc 240

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ggcgggagca tctacaacca gaggttcaag gggaggtca ctctgacgcgt ggatcgctcc	300
aagaacacgc tgtacccca gatgaactct ctcagggccg aggacacggc tgtttactat	360
tgcgcgagga acctgggtcc ttccctctac ttcgactact gggcacagg aaccctggtg	420
accgtcagct ccgcttctac caagggtctt agtgtgtcc ctcttgcctcc cagctctaaa	480
agcacccctcg gtggaaactgc tgctctgggc tgctcggtta aggactactt ccccgaaacc	540
gtgacccgtat ctggaaactc cggegcacett acttctgggc tccacactt cccagccgtc	600
ttacagtctt ctggcctgtt ttctttgagc aegtgcgtga ccgtgcctag cagtagtctg	660
ggcacccaga cctacatctg caacgtcaac cacaaggctt gcaacaccaa ggttgacaag	720
aagggtcgacg ctaagtcgtg cgacaagacg cacggatccc ctggaaagttc ttcaagctct	780
agcagagttgg ctgctcacat cacggaaact cggggtaggt ctaacaccct gtccagcccg	840
aattccaaga acgagaaggc tctgggcagg aagatcaact ctggggagtc cagcagatcc	900
ggtcatacgat ttctgtctaa ctgcacactg agaaacggcg agctgggtat ccatgagaag	960
ggcttctact acatctactc tcagacccag ttcaagtttcc gggaggagat caaggagaac	1020
accaagaacg acaaggcagat ggtgcagttac atctacaagt acaccagcta tccagaccca	1080
atccctgtgtc tgaagtccgc taggaactcc ttgtggagca aagacgccga gtatggcttg	1140
tatagcatct atcaggggagg catcttcgag ctgaaggaga acgacaggat ctgcgtgagc	1200
gtcactaatatc agaggctgtc ccagatggac catgaaggctt ctttcttcgg cgctttctta	1260
gtgggcgggtt ccggaaagcgg tagtggtagt cgctcgccg cacatattac tggcaccgcg	1320
gggagaagta atactttgtc aagtcccaat agcaagaatg agaaggccct gggtcgaaag	1380
atcaatagct gggagtcaag tcggtctggc cacagcttcc tcagtaatct ccatctccga	1440
aatggtaat tggtcataca tgagaagggg ttcttattaca tctatagccaa aactcagttt	1500
aagttcccgag aggagattaa ggagaacacgc aagaatgata agcagatggt tcaatatatt	1560
tacaagtaca ctccctatcc agacccgatc ttgcttatgc agtcagcccg taatagctgt	1620
tggagtaaag atgcagaata cggactctat agtatttacc aagggtggat atttgaactc	1680
aaggagaatg atcgcatatt cgtatctgtc acaaacgaaac gcttgcgtca gatggaccac	1740
gaagcttagtt tcttcggagc attccctgggtt ggccggaaagcg gcagtgaaag cggctctaga	1800
gtagccgccc acataaccgg gacaaggggg cgaagcaaca cgctaaatgc tccataactca	1860
aagaacgaga aagcacttgg acgtaagatc aactcctggg aaagttctcg tagtggcat	1920
tccttcctgtt ccaacccca cttgagaaat ggggagcttg tgattcacga aaaggattc	1980
tactacatct actcccagac acagttcaaa ttcccgagagg aaatcaagga gaataactaag	2040
aacgacaaac agatggtcca gtacatatac aagtacaccc tataccccca tcctatactg	2100
ttgatgaaat ctgcaaggaa ctcttgcgtgg tctaaggacgc ctgagttatgg gttgtactcg	2160
atctaccagg gccggatttt cgagttggaa gagaacgacc gcataattcgt gtcagtaacc	2220
aacgagcgcc ttgttcagat ggaccatgag gcataccctt ttgggtgcctt cctgggtggc	2280
ggtcctggct cagtagcagc cagttcagct tggagtcacc cacagttcga gaagtaatag	2340
gcgcgcgc	2347

<210> SEQ ID NO 51

<211> LENGTH: 761

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: LC-scTRAILR2-SNSN

-continued

<400> SEQUENCE: 51

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Val Leu Leu Trp Val Pro
 1 5 10 15
 Gly Ser Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
 20 25 30
 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
 35 40 45
 Val Ser Ile Gly Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 50 55 60
 Lys Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Ser
 65 70 75 80
 Arg Phe Ser Gly Ser Gly Asp Phe Thr Leu Thr Ile Ser
 85 90 95
 Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr
 100 105 110
 Ile Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 115 120 125
 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 130 135 140
 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 145 150 155 160
 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 165 170 175
 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 180 185 190
 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 195 200 205
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 210 215 220
 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Ser Pro Gly Ser Ser
 225 230 235 240
 Ser Ser Ser Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg
 245 250 255
 Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly
 260 265 270
 Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu
 275 280 285
 Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly
 290 295 300
 Phe Tyr Tyr Ile Tyr Ser Gln Thr Gln Phe Lys Phe Arg Glu Glu Ile
 305 310 315 320
 Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys
 325 330 335
 Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn
 340 345 350
 Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln
 355 360 365
 Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val
 370 375 380
 Thr Asn Glu Arg Leu Leu Gln Met Asp His Glu Ala Ser Phe Phe Gly
 385 390 395 400
 Ala Phe Leu Val Gly Gly Ser Gly Ser Gly Asn Gly Ser Arg Val Ala

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405	410	415
Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro		
420	425	430
Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu		
435	440	445
Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn		
450	455	460
Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln		
465	470	475
480		
Thr Gln Phe Lys Phe Arg Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp		
485	490	495
Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro		
500	505	510
Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala		
515	520	525
Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys		
530	535	540
Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu Arg Leu Leu Gln		
545	550	555
560		
Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly Ser		
565	570	575
Gly Ser Gly Asn Gly Ser Arg Val Ala Ala His Ile Thr Gly Thr Arg		
580	585	590
Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala		
595	600	605
Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser		
610	615	620
Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu		
625	630	635
640		
Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Gln Phe Lys Phe Arg Glu		
645	650	655
Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile		
660	665	670
Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala		
675	680	685
Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile		
690	695	700
Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val		
705	710	715
720		
Ser Val Thr Asn Glu Arg Leu Leu Gln Met Asp His Glu Ala Ser Phe		
725	730	735
Phe Gly Ala Phe Leu Val Gly Gly Pro Gly Ser Ser Ser Ser Ser		
740	745	750
Ala Trp Ser His Pro Gln Phe Glu Lys		
755	760	

<210> SEQ_ID NO 52
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: linker sequence

<400> SEQUENCE: 52

Gly Ser Gly Ser Gly Ser Gly Ser

-continued

1 5

```
<210> SEQ ID NO 53
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: linker sequence

<400> SEQUENCE: 53
```

Gly Ser Gly Ser Gly Asn Gly Ser
1 5

```
<210> SEQ ID NO 54
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: linker sequence figure 21A
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (0)..(0)
<223> OTHER INFORMATION: linker sequence figure 21A
```

<400> SEQUENCE: 54

Gly Ser Gly Asn Gly Ser Gly Ser
1 5

```
<210> SEQ ID NO 55
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Linker1 [DKTHTG(S)a(G)b; (a=0-5; b=0 or 1)],
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker1 [DKTHTG(S)a(G)b; (a=0-5; b=0 or 1)], example1, when a=5 and b=1
```

<400> SEQUENCE: 55

Asp Lys Thr His Thr Gly Ser Ser Ser Ser Gly
1 5 10

```
<210> SEQ ID NO 56
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 28, Linker1, [DKTHTG(S)a(G)b; (a=0-5; b=0 or 1)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker1 [DKTHTG(S)a(G)b; (a=0-5; b=0 or 1)], example2, when a=5 and b=0
```

<400> SEQUENCE: 56

Asp Lys Thr His Thr Gly Ser Ser Ser Ser
1 5 10

```
<210> SEQ ID NO 57
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 28, Linker2, [DKTHTGS(S)a(GS)bG(S)c; (a,b=0, 1-6; c=0 or 1)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker2 [DKTHTGS(S)a(GS)bG(S)c; (a,b=0, 1-6; c=0 or 1)], example-1, when a=6 and b=0 and c=1
```


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<210> SEQ_ID NO 62
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 28, Linker3, [DKTG(S)a(G)b; (a=0-5; b=0
    or1)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker3 [DKTG(S)a(G)b; (a=0-5; b=0 or1)],
    example1, when a=5 and b=1

<400> SEQUENCE: 62

Asp Lys Thr Gly Ser Ser Ser Ser Gly
1          5           10

```

```

<210> SEQ_ID NO 63
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 28, Linker4, [DKTG(S)a(GS)bG(S)c;
    (a,b =0, 1-6; c=0 or 1)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker4 [DKTG(S)a(GS)bG(S)c;
    (a,b =0, 1-6; c=0 or 1)], example1, when a=6 and b=0 and c=1

<400> SEQUENCE: 63

Asp Lys Thr Gly Ser Ser Ser Ser Ser Gly Ser
1          5           10

```

```

<210> SEQ_ID NO 64
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 28, Linker4, [DKTG(S)a(GS)bG(S)c;
    (a,b =0, 1-6; c=0 or 1)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker4 [DKTG(S)a(GS)bG(S)c; (a,b =0, 1-6;
    c=0 or 1)], example2, when a=6 and b=1 and c=1

<400> SEQUENCE: 64

Asp Lys Thr Gly Ser Ser Ser Ser Ser Ser Gly Ser
1          5           10           15

```

```

<210> SEQ_ID NO 65
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 28, Linker4, [DKTG(S)a(GS)bG(S)c; (a,b =0,
    1-6; c=0 or 1)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker4 [DKTG(S)a(GS)bG(S)c; (a,b =0, 1-6; c=0
    or 1)], example3, when a=5 and b=1 and c=1

<400> SEQUENCE: 65

```

```

Asp Lys Thr Gly Ser Ser Ser Ser Ser Gly Ser
1          5           10

```

```

<210> SEQ_ID NO 66
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: page 28, Linker4, [DKTG(S)a(GS)bG(S)c; (a,b =0, 1-6; c=0 or 1)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker4 [DKTG(S)a(GS)bG(S)c; (a,b =0, 1-6; c=0 or 1)], example4, when a=5 and b=0 and c=1

<400> SEQUENCE: 66

Asp Lys Thr Gly Ser Ser Ser Ser Ser Gly Ser
1 5 10

<210> SEQ ID NO 67
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 28, Linker4, [DKTG(S)a(GS)bG(S)c; (a,b =0, 1-6; c=0 or 1)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker4 [DKTG(S)a(GS)bG(S)c; (a,b =0, 1-6; c=0 or 1)], example5, when a=3 and b=0 and c=1

<400> SEQUENCE: 67

Asp Lys Thr Gly Ser Ser Ser Ser Gly Ser
1 5 10

<210> SEQ ID NO 68
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 28, Linker5, [SSG(S)a(GS)bG(S)c; (a, b =0, 1-6; c=0 or 1)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker5 [SSG(S)a(GS)bG(S)c; (a, b =0, 1-6; c=0 or 1)], example1, when a=1 and b=1 and c=1

<400> SEQUENCE: 68

Ser Ser Gly Ser Gly Ser Gly Ser
1 5

<210> SEQ ID NO 69
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 28, Linker5, [SSG(S)a(GS)bG(S)c; (a, b =0, 1-6; c=0 or 1)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker5 [SSG(S)a(GS)bG(S)c; (a, b =0, 1-6; c=0 or 1)], example2, when a=5 and b=1 and c=1

<400> SEQUENCE: 69

Ser Ser Gly Ser Ser Ser Ser Ser Gly Ser Gly Ser
1 5 10

<210> SEQ ID NO 70
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 28, Linker6, [SS(GGGG)aG(s)b, (a=0, 1-4, b=0 or 1)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker6 [SS(GGGG)aG(s)b, (a=0, 1-4, b=0 or 1)], example1, when a=1 and b=1

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<400> SEQUENCE: 70

Ser Ser Gly Gly Ser Gly Ser
1 5

<210> SEQ ID NO 71
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 28, Linker6, [SS(GGGS)aG(s)b, (a=0, 1-4,
b=0 or 1)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker6 [SS(GGGS)aG(s)b, (a=0, 1-4, b=0 or 1)],
example2, when a=2 and b=1

<400> SEQUENCE: 71

Ser Ser Gly Gly Ser Gly Gly Ser Gly Ser
1 5 10

<210> SEQ ID NO 72
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 28, Linker7, [GSPGSSSSSS(G)a, (a=0 or 1)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker7[GSPGSSSSSS(G)a, (a=0 or 1)], example1,
when a=1

<400> SEQUENCE: 72

Gly Ser Pro Gly Ser Ser Ser Ser Ser Gly
1 5 10

<210> SEQ ID NO 73
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 32, Linker8,
[GG(P/S)a(GS)b(G/S)cKSCDKTHTCPPCPAPE, (a=0 or 1; b=0-8; c=0-8)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker8 [GG(P/S)a(GS)b(G/S)cKSCDKTHTCPPCPAPE,
(a=0 or 1; b=0-8; c=0-8)], example1, when a=1 and b=1 and c=1

<400> SEQUENCE: 73

Gly Gly Pro Gly Ser Ser Lys Ser Cys Asp Lys Thr His Thr Cys Pro
1 5 10 15

Pro Cys Pro Ala Pro Glu
20

<210> SEQ ID NO 74
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 32, Linker8,
[GG(P/S)a(GS)b(G/S)cKSCDKTHTCPPCPAPE, (a=0 or 1; b=0-8; c=0-8)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker8 [GG(P/S)a(GS)b(G/S)cKSCDKTHTCPPCPAPE,
(a=0 or 1; b=0-8; c=0-8)], example2, when a=1 and b=1 and c=1

<400> SEQUENCE: 74

Gly Gly Ser Gly Ser Ser Lys Ser Cys Asp Lys Thr His Thr Cys Pro
1 5 10 15

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Pro Cys Pro Ala Pro Glu
20

```
<210> SEQ ID NO 75
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 32, Linker8,
  [GG(P/S)a(GS)b(G/S)cKSCDKTHTCPPCPAPE; (a=0 or 1; b=0-8; c=0-8)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker8 [GG(P/S)a(GS)b(G/S)cKSCDKTHTCPPCPAPE;
  (a=0 or 1; b=0-8; c=0-8)], example3, when a=1 and b=1 and c=6
```

<400> SEQUENCE: 75

Gly	Gly	Pro	Gly	Ser	Ser	Ser	Ser	Ser	Lys	Ser	Cys	Asp	Lys
1													15

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
20 25

```
<210> SEQ ID NO 76
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 32, Linker8,
  [GG(P/S)a(GS)b(G/S)cKSCDKTHTCPPCPAPE; (a=0 or 1; b=0-8; c=0-8)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker8 [GG(P/S)a(GS)b(G/S)cKSCDKTHTCPPCPAPE;
  (a=0 or 1; b=0-8; c=0-8)], example4, when a=1 and b=1 and c=6
```

<400> SEQUENCE: 76

Gly	Gly	Ser	Gly	Ser	Ser	Ser	Ser	Ser	Lys	Ser	Cys	Asp	Lys
1													15

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
20 25

```
<210> SEQ ID NO 77
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 32, Linker8,
  [GG(P/S)a(GS)b(G/S)cKSCDKTHTCPPCPAPE; (a=0 or 1; b=0-8; c=0-8)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker8 [GG(P/S)a(GS)b(G/S)cKSCDKTHTCPPCPAPE;
  (a=0 or 1; b=0-8; c=0-8)], example5, when a=1 and b=1 and c=8
```

<400> SEQUENCE: 77

Gly	Gly	Pro	Gly	Ser	Ser	Ser	Ser	Ser	Ser	Lys	Ser	Cys
1												
												15

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
20 25

```
<210> SEQ ID NO 78
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 32, Linker8,
  [GG(P/S)a(GS)b(G/S)cKSCDKTHTCPPCPAPE; (a=0 or 1; b=0-8; c=0-8)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker8 [GG(P/S)a(GS)b(G/S)cKSCDKTHTCPPCPAPE;
  (a=0 or 1; b=0-8; c=0-8)], example6, when a=1 and b=1 and c=8
```

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<400> SEQUENCE: 78

Gly	Gly	Ser	Gly	Ser	Lys	Ser	Cys						
1												15	

Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	
												25	

<210> SEQ ID NO 79

<211> LENGTH: 24

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: page 32, Linker9,
[GG(P/S)a(GSSGS)bGS(G/S)cDKTHTCPPCPAPE; (a=0 or 1; b=0-8; c=0-8)]

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<223> OTHER INFORMATION: Linker9 [GG(P/S)a(GSSGS)bGS(G/S)cDKTHTCPPCPAPE;
(a=0 or 1; b=0-8; c=0-8)], example1, when a=1 and b=1 and c=1

<400> SEQUENCE: 79

Gly	Gly	Pro	Gly	Ser	Ser	Gly	Ser	Ser	Asp	Lys	Thr	His	Thr
1											15		

Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu					
											20	

<210> SEQ ID NO 80

<211> LENGTH: 23

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: page 32, Linker9,
[GG(P/S)a(GSSGS)bGS(G/S)cDKTHTCPPCPAPE; (a=0 or 1; b=0-8; c=0-8)]

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<223> OTHER INFORMATION: Linker9 [GG(P/S)a(GSSGS)bGS(G/S)cDKTHTCPPCPAPE;
(a=0 or 1; b=0-8; c=0-8)], example1, when a=1 and b=1 and c=0

<400> SEQUENCE: 80

Gly	Gly	Pro	Gly	Ser	Ser	Gly	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys
1											15			

Pro	Pro	Cys	Pro	Ala	Pro	Glu					
										20	

<210> SEQ ID NO 81

<211> LENGTH: 21

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: page 32, Linker10,
[GG(P/S)a(S)b(GS)c(G/S)dDKTHTCPPCPAPE; (a=0 or 1; b=0-8; c=0-8;
d=0-8)]

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<223> OTHER INFORMATION: Linker10 [GG(P/S)a(S)b(GS)c(G/S)dDKTHTCPPCPAPE;
(a=0 or 1; b=0-8;
c=0-8; d=0-8)], example1, when a=1 and b=3 and c=1 and d=0

<400> SEQUENCE: 81

Gly	Gly	Pro	Ser	Ser	Ser	Gly	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro
1											15					

Cys	Pro	Ala	Pro	Glu							
										20	

<210> SEQ ID NO 82

<211> LENGTH: 25

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

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<223> OTHER INFORMATION: page 32, Linker10,
 [GG(P/S)a(S)b(GS)c(G/S)dDKHTCPPCPAPE; (a=0 or 1; b=0-8; c=0-8;
 d=0-8)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker10 [GG(P/S)a(S)b(GS)c(G/S)dDKHTCPPCPAPE;
 (a=0 or 1; b=0-8;
 c=0-8; d=0-8)], example2, when a=1and b=7 and c=1 and d=0

<400> SEQUENCE: 82

Gly	Gly	Ser	Gly	Ser	Asp	Lys	Thr	His						
1									5		10		15	
Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu						
				20				25						

<210> SEQ ID NO 83
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 34, Linker11, [(S)a(GS)bG(S)c; (a,b=0,1-6;
 c=0 or 1)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker11 [(S)a(GS)bG(S)c; (a,b=0,1-6;
 c=0 or 1)], example1, when a=1and b=5 and c=1

<400> SEQUENCE: 83

Ser	Gly	Ser									
1								5		10	

<210> SEQ ID NO 84
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 34, Linker11, [(S)a(GS)bG(S)c; (a,b=0,1-6;
 c=0 or 1)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker11 [(S)a(GS)bG(S)c;
 (a,b=0,1-6; c=0 or 1)], example2, when a=6and b=2 and c=1

<400> SEQUENCE: 84

Ser	Ser	Ser	Ser	Ser	Ser	Gly	Ser	Gly	Ser		
1								5		10	

<210> SEQ ID NO 85
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 34, Linker11, [(S)a(GS)bG(S)c; (a,b=0,1-6;
 c=0 or 1)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker11 [(S)a(GS)bG(S)c; (a,b=0,1-6;
 c=0 or 1)], example3, when a=6 and b=5 and c=1

<400> SEQUENCE: 85

Ser	Ser	Ser	Ser	Ser	Ser	Gly	Ser	Gly	Ser	Gly	Ser	
1								5		10	15	

<210> SEQ ID NO 86
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 34, Linker12, [S(GGGS)aGb(S)c;
 (a,b=0,1-6; c=0 or 1)]

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<220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <223> OTHER INFORMATION: Linker12 [S(GGGS)aGb(S)c; (a,b=0,1-6;
 c=0 or 1)], example1, when a=2 and b=1 and c=1

<400> SEQUENCE: 86

Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Ser
1				5				10		

<210> SEQ ID NO 87
 <211> LENGTH: 14
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: page 35, Linker13, [DKTHTCPGSS(GS)aG(S)b;
 (a=0,1-6; b=0 or 1)]
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <223> OTHER INFORMATION: Linker13 [DKTHTCPGSS(GS)aG(S)b; (a=0,1-6;
 b=0 or 1)], example1, when a=1 and b=1

<400> SEQUENCE: 87

Asp	Lys	Thr	His	Thr	Cys	Pro	Gly	Ser	Ser	Gly	Ser
1				5				10			

<210> SEQ ID NO 88
 <211> LENGTH: 12
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: page 35, Linker14, [DKTHTCPGSSaG(S)b; (a=0,1-6;
 b=0 or 1)]
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <223> OTHER INFORMATION: Linker14 [DKTHTCPGSSaG(S)b; (a=0,1-6;
 b=0 or 1)], example1, when a=1 and b=1

<400> SEQUENCE: 88

Asp	Lys	Thr	His	Thr	Cys	Pro	Gly	Ser	Ser	Gly	Ser
1				5				10			

<210> SEQ ID NO 89
 <211> LENGTH: 15
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: page 35, Linker15, [DKTHTC(GSSGS)aGSG(S)b;
 (a=0,1-6; b=0 or 1)]
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <223> OTHER INFORMATION: Linker15 [DKTHTC(GSSGS)aGSG(S)b; (a=0,1-6;
 b=0 or 1)], example1, when a=1 and b=1

<400> SEQUENCE: 89

Asp	Lys	Thr	His	Thr	Cys	Gly	Ser	Ser	Gly	Ser	Gly	Ser
1				5				10		15		

<210> SEQ ID NO 90
 <211> LENGTH: 13
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: page 35, Linker16, [DKTHTCGSS(GS)aG(S)b;
 (a=0,1-6; b=0 or 1)]
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <223> OTHER INFORMATION: Linker16 [DKTHTCGSS(GS)aG(S)b; (a=0,1-6;
 b=0 or 1)], example1, when a=1 and b=1

<400> SEQUENCE: 90

-continued

Asp Lys Thr His Thr Cys Gly Ser Ser Gly Ser
1 5 10

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<210> SEQ ID NO 91
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 35, Linker17, [DKTHTCGSSaG(S)b; (a=0,1-6;
b=0 or 1)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker17 [DKTHTCGSSaG(S)b; (a=0,1-6;
b=0 or 1)], example1, when a=1 and b=1

<400> SEQUENCE: 91
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Asp Lys Thr His Thr Cys Gly Ser Ser Gly Ser
1 5 10

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<210> SEQ ID NO 92
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 35, Linker18, [DKTHTC(GSSGS)aGS(G)b;
(a=0,1-6; b=0 or 1)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker18 [DKTHTC(GSSGS)aGS(G)b; (a=0,1-6;
b=0 or 1)], example1, when a=1 and b=1

<400> SEQUENCE: 92
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Asp Lys Thr His Thr Cys Gly Ser Ser Gly Ser Gly
1 5 10

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<210> SEQ ID NO 93
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 35, Linker19, [DKTHTCPPCPGSSGSGSGS(G)b;
(b=0 or 1)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker19 [DKTHTCPPCPGSSGSGSGS(G)b; (b=0 or 1)],
example1, when a=1 and b=1

<400> SEQUENCE: 93
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Asp Lys Thr His Thr Cys Pro Pro Cys Pro Gly Ser Ser Gly Ser Gly
1 5 10 15

Ser Gly Ser Gly
20

```
<210> SEQ ID NO 94
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: PAGE 35, LINKER20, [DKTHTCPPCP(GSSGS)AGS(G)B;
(A=0, 1-6; B=0 OR 1)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker20 [DKTHTCPPCP(GSSGS)aGS(G)b; (a=0, 1-6;
b=0 or 1)], example1, when a=1 and b=1

<400> SEQUENCE: 94
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Asp Lys Thr His Thr Cys Pro Pro Cys Pro Gly Ser Ser Gly Ser Gly
1 5 10 15

Ser Gly

-continued

<210> SEQ_ID NO 95
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 35, Linker21, [DKTHTCPPCPGSS (GS) aGS (G) b;
(a=0, 1-6; b=0 or 1)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker21 [DKTHTCPPCPGSS (GS) aGS (G) b; (a=0, 1-6;
b=0 or 1)], example1, when a=3 and b=1

<400> SEQUENCE: 95

Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Gly	Ser	Ser	Gly	Ser	Gly
1					5				10				15		
Ser Gly Ser Gly Ser Gly															
20															

<210> SEQ_ID NO 96
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 35, Linker22, [DKTHTCPPCPGSSaGS (G) b;
(a=0, 1-6; b=0 or 1)]
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Linker22 [DKTHTCPPCPGSSaGS (G) b; (a=0, 1-6;
b=0 or 1)], example1, when a=1 and b=1

<400> SEQUENCE: 96

Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Gly	Ser	Ser	Gly	Ser	Gly
1					5				10				15		

<210> SEQ_ID NO 97
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 33, table 2
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: FC01_linker [(G)GSPGSSSSSGSDKTH]

<400> SEQUENCE: 97

Gly	Gly	Ser	Pro	Gly	Ser	Ser	Ser	Ser	Ser	Gly	Ser	Asp	Lys	Thr
1					5				10				15	

His

<210> SEQ_ID NO 98
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 33, table 2
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: FC02_linker [(G)GSPGSSSSGSDKTH]

<400> SEQUENCE: 98

Gly	Gly	Ser	Pro	Gly	Ser	Ser	Ser	Ser	Gly	Ser	Asp	Lys	Thr	His
1					5				10				15	

<210> SEQ_ID NO 99
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

-continued

<220> FEATURE:
<223> OTHER INFORMATION: page 33, table 2
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: FC03_linker [(G)GSPGSSGSDKTH]

<400> SEQUENCE: 99

Gly	Gly	Ser	Pro	Gly	Ser	Ser	Gly	Ser	Asp	Lys	Thr	His
1				5					10			

<210> SEQ ID NO 100
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 33, table 2
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: FC04_linker [(G)GSPGSSDKTH]

<400> SEQUENCE: 100

Gly	Gly	Ser	Pro	Gly	Ser	Ser	Asp	Lys	Thr	His
1				5				10		

<210> SEQ ID NO 101
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 33, line 9
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: flexible linker element connecting Fc-domain with a C-terminal Strep-Tag-II

<400> SEQUENCE: 101

Ser	Ser	Ser	Ser	Ser	Ser	Ala
1				5		

<210> SEQ ID NO 102
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: page 33, line 9
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Strep-tag-II sequence

<400> SEQUENCE: 102

Trp	Ser	His	Pro	Gln	Phe	Glu	Lys
1				5			

What is claimed is:

1. A single-chain fusion polypeptide comprising:
 - (i) a first soluble TNF-related apoptosis-inducing ligand (TRAIL) cytokine domain,
 - (ii) a first peptide linker,
 - (iii) a second soluble TRAIL cytokine domain,
 - (iv) a second peptide linker, and
 - (v) a third soluble TRAIL cytokine domain,
- wherein each of the soluble TRAIL domains lacks a stalk region and the first and the second peptide linkers independently have a length of 3-8 amino acids.
2. The polypeptide of claim 1, wherein the second and/or third soluble TRAIL domain is an N-terminally shortened domain which optionally comprises amino acid sequence mutations.

3. The polypeptide of claim 1, wherein at least one of the soluble TRAIL domains has an N-terminal sequence which starts at amino acid Gln120, Arg121, or Val122 of human TRAIL (SEQ ID NO: 10), and the Arg121 is optionally replaced by a neutral amino acid of serine or glycine.

4. The polypeptide of claim 3, wherein at least one of the soluble TRAIL domains has an N-terminal sequence selected from

- 60 (a) Arg121-Val122-Ala123 and
- (b) (Gly/Ser)121-Val122-Ala123.

5. The polypeptide of claim 3, wherein at least one of the soluble TRAIL domains ends with amino acid Gly281 of human TRAIL and optionally comprises one or more mutations at positions R130, G160, H168, R170, H177, Y189, R191, Q193, E195, N199, K201, Y213, T214, S215, H264, I266, D267 or D269.

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6. The polypeptide of claim 1, which additionally comprises an N-terminal signal peptide domain.
7. The polypeptide of claim 6, wherein the N-terminal signal peptide domain comprises a protease cleavage site.
8. The polypeptide of claim 1, which additionally comprises a further domain at the N-terminal and/or C-terminal end. 5
9. The polypeptide of claim 8, wherein the further domain is a Fab or Fc fragment domain.
10. A pharmaceutical composition comprising the fusion polypeptide of claim 1 and a pharmaceutically acceptable carrier, diluent and/or adjuvant. 10
11. The polypeptide of claim 1, wherein the first and second peptide linkers are independently glycine-serine linkers.
12. The polypeptide of claim 11, wherein the glycine/ 15 serine linkers comprises substituted asparagine residues.
13. The polypeptide of claim 9, wherein the further domain is a Fc fragment domain at the C-terminal end.
14. The polypeptide of claim 9, wherein the further domain is an Fc fragment domain at the N-terminal end. 20
15. A dimer comprising two polypeptides of claim 13, fused via disulfide bridges between the Fc fragment domains.
16. A dimer comprising two polypeptides of claim 14, fused via disulfide bridges between the Fc fragment domains.
17. An isolated nucleic acid molecule encoding the fusion 25 polypeptide of claim 1.
18. An isolated host cell or a non-human organism transformed or transfected with the nucleic acid molecule of claim 17.

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